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REMARKS

I. Introduction

Applicants respectfully request reconsideration of the present application in view of the foregoing amendments and in view of the reasons that follow.

A. Status of the Claims

Claims 6, 35 and 36 are currently being amended.

This amendment adds, changes and/or deletes claims in this application. A detailed listing of all claims that are, or were, in the application, irrespective of whether the claim(s) remain under examination in the application, is presented, with an appropriate defined status identifier.

Support for the amendments to claims 6, 35 and 36 is found throughout the specification. Exemplary support for “PP2C activity” is found in the specification in the paragraph bridging pages 54 and 55 and in Tables 1, 2 and 3.

Upon entry of this Amendment, claims 6 and 34-37 will remain pending in the application.

B. Interview

Applicants would like to thank Examiner Slobodyansky for her time and insights during the interview with Applicants’ representative on March 24, 2004. During the interview, the Examiner indicated that a sequence alignment showing high sequence similarity between SEQ ID NO: 8 and a sequence with PP2C activity would be useful for overcoming the rejection under 35 U.S.C. § 101. The Examiner indicated that the rejection under 35 U.S.C. § 112, first paragraph, would be overcome if Applicants amended the claims by replacing the term “phosphatase activity” with “PP2C activity.” The Examiner also indicated that deleting the term “and a catalytic domain” from claims 36 and 37 should overcome the rejection of these claims under 35 U.S.C. § 112, second paragraph.

II. Issues Raised By Examiner In Advisory Action

A. Claim Rejections – 35 U.S.C. § 101

The Examiner asserts that Applicants did not provide any evidence that a polypeptide of SEQ ID NO:8 has PP2C activity or that SEQ ID NO: 8 is highly homologous to a polypeptide for which such activity has been shown. During a telephone interview with the Examiner on March 24, 2004, Applicants brought to the Examiner's attention a NCBI Conserved Domain Search analysis which shows the alignment of SEQ ID NO:8 with sequences from the database and the overall percent identity between SEQ ID NO:8 and sequences from the database (*see* Exhibit 1 attached herewith). The Examiner indicated that a sequence alignment showing high sequence similarity between SEQ ID NO: 8 and a sequence with PP2C activity would be useful for overcoming the rejection under 35 U.S.C. § 101.

Attached as Exhibit 2 is an excerpt from the NCBI Conserved Domain Search analysis containing the alignment of SEQ ID NO:8 with GI 39573724 (see first entry on page 2 of the NCBI Conserved Domain Search analysis). GI 39573724, mouse PP2C η , shares 89% sequence identity with SEQ ID NO:8. Attached herewith as Exhibit 3 is Komaki, et al., *Biochim. Biophys. Acta*, 2003, 1630(2-3):130-137, which details the cloning of PP2C η .

Additionally, the paragraph bridging pages 54 and 55, as well as Tables 1, 2 and 3 of the specification, establish that the polypeptide of SEQ ID NO:8 is a PP2C.

In view of these arguments and evidence, the polypeptide of SEQ ID NO:8 is a PP2C.

B. Claim Rejections - 35 U.S.C. § 112, First Paragraph

The Examiner asserts that the term "phosphatase activity" encompasses various activities. Applicants do not agree with the Examiner. However, in order to expedite prosecution, Applicants have amended the claims by replacing the term "phosphatase activity" with "PP2C activity." Support for this amendment is found in the specification in the paragraph bridging pages 54 and 55 and in Tables 1, 2 and 3.

C. Claim Rejections - 35 U.S.C. § 112, Second Paragraph

The Examiner asserts that in claim 33, the difference between the recited domains is unclear. Applicants respectfully disagree with the Examiner. However, to expedite prosecution, Applicants have canceled claim 33. The cancellation of claims does not constitute acquiescence in the propriety of any rejection set forth by the Examiner. Applicants reserve the right to pursue the subject matter of the canceled claims in subsequent divisional applications.

The Examiner also asserts that amending claims 36 and 37 to recite “and a catalytic domain” renders the claims further confusing because it is allegedly unclear whether a contiguous or hybrid sequence is claimed. Applicants do not agree with the Examiner. However, in order to expedite prosecution, Applicants have deleted the term “and a catalytic domain” from claims 36 and 37.

D. Claim Rejections - 35 U.S.C. § 103

The Examiner asserts that claim 33 is obvious in view of Hillier because the EST disclosed by Hillier can be construed as encoding some domains (i.e., the C-terminal domain). Applicants respectfully disagree with the Examiner. However, to expedite prosecution, Applicants have canceled claim 33. The cancellation of claims does not constitute acquiescence in the propriety of any rejection set forth by the Examiner. Applicants reserve the right to pursue the subject matter of the canceled claims in subsequent divisional applications.

III. CONCLUSION

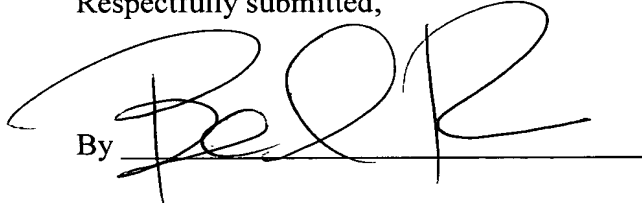
The present application is now in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested.

Applicants believes the application is in condition for allowance. However, in order to maintain pendency of the application, Applicants are filing a Notice of Appeal.

The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

The Commissioner is hereby authorized to charge any additional fees which may be required regarding this application under 37 C.F.R. §§ 1.16-1.17, or credit any overpayment, to Deposit Account No. 19-0741. Should no proper payment be enclosed herewith, as by a check being in the wrong amount, unsigned, post-dated, otherwise improper or informal or even entirely missing, the Commissioner is authorized to charge the unpaid amount to Deposit Account No. 19-0741. If any extensions of time are needed for timely acceptance of papers submitted herewith, Applicant(s) hereby petition(s) for such extension under 37 C.F.R. §1.136 and authorizes payment of any such extensions fees to Deposit Account No. 19-0741.

Respectfully submitted,

By 

Beth A. Burrous
Attorney for Applicant
Registration 35,087

Date April 29, 2004

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BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
 Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
 "Gapped BLAST and PSI-BLAST: a new generation of protein database search
 programs", Nucleic Acids Res. 25:3389-3402.

RID: 1072110441-10830-135706414391.BLASTQ4

Query=

(459 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

1,581,064 sequences; 518,058,112 total letters

If you have any problems or questions with the results of this search please
 refer to the BLAST FAQs

Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Sequences producing significant alignments:	Score (bits)	E Value
gi 39573724 ref NP_945149.1 protein phosphatase 2C eta iso...	704	0.0
gi 26338027 dbj BAC32699.1 unnamed protein product [Mus mu...	544	e-153
gi 21389471 ref NP_653242.1 hypothetical protein FLJ32332 ...	512	e-144
gi 16307111 gb AAH09644.1 FLJ32332 protein [Homo sapiens]	499	e-140
gi 12856386 dbj BAB30649.1 unnamed protein product [Mus mu...	445	e-124
gi 28892713 ref NP_795893.1 RIKEN cDNA A430075L18 gene [Mu...	357	2e-97
gi 29611652 ref NP_082258.1 protein phosphatase 2a, cataly...	335	1e-90
gi 33873319 gb AAH11803.2 MGC19531 protein [Homo sapiens]	334	2e-90
gi 31127152 gb AAH52910.1 Unknown (protein for IMAGE:30075...	332	1e-89
gi 34859725 ref XP_215663.2 similar to protein phosphatase...	327	3e-88
gi 34526234 dbj BAC85206.1 unnamed protein product [Homo s...	311	2e-83
gi 39930533 ref NP_005158.4 hypothetical protein MGC19531 ...	271	3e-71
gi 17539110 ref NP_502329.1 protein phosphatase 2C-like (4...	261	2e-68
gi 31203861 ref XP_310879.1 ENSANGP00000008051 [Anopheles ...	256	6e-67
gi 19920426 ref NP_608468.1 CG17598-PA [Drosophila melanog...	255	1e-66
gi 3242077 emb CAA05875.1 protein phosphatase 2C [Arabidop...	89	1e-16
gi 7768151 emb CAB90633.1 protein phpsphatase 2C (PP2C) [F...	88	3e-16
gi 30685388 ref NP_173199.2 protein phosphatase 2C (PP2C) ...	88	3e-16
gi 26452332 dbj BAC43252.1 unknown protein [Arabidopsis th...	88	3e-16
gi 33309516 gb AAQ03211.1 protein phosphatase 2C [Prunus a...	86	2e-15
gi 21902025 dbj BAC05575.1 protein phosphatase 2C-like pro...	81	3e-14
gi 15222398 ref NP_172223.1 protein phosphatase 2C (PP2C),...	80	7e-14

gi 8778461 gb AAF79469.1	F1L3.26 [Arabidopsis thaliana]	79	1e-13
gi 3643082 gb AAC36697.1	protein phosphatase-2C; PP2C [Mes...	79	2e-13
gi 15229745 ref NP_187748.1	protein phosphatase 2C (PP2C),...	79	2e-13
gi 609658 gb AAA67321.1	protein phosphatase 2C (ptc3+)	77	7e-13
gi 16226419 gb AAL16163.1	AT5g59220/mnc17_110 [Arabidopsis...	77	1e-12
gi 15237839 ref NP_200730.1	protein phosphatase 2C (PP2C),...	77	1e-12
gi 15236110 ref NP_194338.1	protein phosphatase ABI1 [Arab...	76	1e-12
gi 509419 emb CAA55484.1	ABI1 [Arabidopsis thaliana]	76	1e-12
gi 10432446 emb CAC10358.1	protein phosphatase 2C [Nicotia...	76	1e-12
gi 14334800 gb AAK59578.1	putative protein phosphatase ABI...	76	1e-12
gi 19113999 ref NP_593087.1	protein phosphatase 2c homolog...	76	1e-12
gi 15227078 ref NP_180499.1	protein phosphatase 2C (PP2C),...	75	2e-12
gi 38109901 gb EAA55700.1	hypothetical protein MG01351.4 [...	75	2e-12
gi 15242022 ref NP_200515.1	protein phosphatase 2C, ABI2 [...	75	3e-12
gi 32406686 ref XP_323956.1	hypothetical protein [Neurospo...	75	3e-12
gi 25352225 pir F86206	hypothetical protein [imported] - A...	75	4e-12
gi 17555234 ref NP_497949.1	protein phosphatase 2C, possib...	74	4e-12
gi 4336436 gb AAD17805.1	protein phosphatase type 2C [Lotu...	71	4e-11
gi 32492311 emb CAE03844.1	OSJNBb0089K06.2 [Oryza sativa (...	70	9e-11
gi 39591591 emb CAE71168.1	Hypothetical protein CBG18025 [...	69	1e-10
gi 6478146 emb CAB61839.1	putative serine/threonine phosph...	69	1e-10
gi 15220548 ref NP_176948.1	protein phosphatase 2C (PP2C),...	69	2e-10
gi 34908256 ref NP_915475.1	putative protein phosphatase 2...	68	4e-10
gi 30693757 ref NP_175057.2	protein phosphatase 2C (PP2C),...	67	8e-10
gi 34902050 ref NP_912371.1	putative Serine/threonine phos...	67	1e-09
gi 26331022 dbj BAC29241.1	unnamed protein product [Mus mu...	66	1e-09
gi 34857062 ref XP_227247.2	similar to protein phosphatase...	66	1e-09
gi 31197933 ref XP_307914.1	ENSANGP00000021879 [Anopheles ...	65	2e-09
gi 18417190 ref NP_567808.1	protein phosphatase 2C (PP2C),...	65	3e-09
gi 29568126 gb AAO43055.1	protein phosphatase 2C epsilon [...	65	3e-09
gi 18395099 ref NP_564165.1	protein phosphatase 2C (PP2C),...	65	3e-09
gi 30689144 ref NP_194903.2	protein phosphatase 2C (PP2C),...	64	6e-09
gi 15242182 ref NP_199989.1	protein phosphatase 2C (PP2C),...	64	9e-09
gi 15225656 ref NP_181547.1	protein phosphatase 2C (PP2C),...	63	9e-09
gi 7487243 pir T00750	probable protein phosphatase 2C [imp...	63	1e-08
gi 19387276 gb AAL87187.1	putative protein phosphatase 2C ...	63	1e-08
gi 21537096 gb AAM61437.1	protein phosphatase type 2C, put...	62	2e-08
gi 7486331 pir T05095	hypothetical protein F28M20.60 - Ara...	62	3e-08
gi 38345197 emb CAE02890.2	OSJNBa0015K02.7 [Oryza sativa (...	62	3e-08
gi 32488822 emb CAE03557.1	OSJNBa0085I10.2 [Oryza sativa (...	61	4e-08
gi 18399423 ref NP_565480.1	protein phosphatase 2C (PP2C),...	60	7e-08
gi 31220270 ref XP_316899.1	ENSANGP00000011103 [Anopheles ...	60	8e-08
gi 19920896 ref NP_609154.1	CG7115-PB [Drosophila melanoga...	60	8e-08
gi 34913678 ref NP_918186.1	OSJNBa0062A24.10 [Oryza sativa...	60	1e-07
gi 28393269 gb AAO42063.1	putative protein phosphatase 2C ...	59	1e-07
gi 31216428 ref XP_316230.1	ENSANGP00000017684 [Anopheles ...	59	2e-07
gi 29248941 gb EAA40463.1	GLP_159_22507_21425 [Giardia lam...	59	2e-07
gi 26390163 dbj BAC25853.1	unnamed protein product [Mus mu...	58	4e-07
gi 15236548 ref NP_194914.1	protein phosphatase 2C (PP2C),...	58	5e-07
gi 21539551 gb AAM53328.1	putative protein phosphatase typ...	58	5e-07
gi 38105092 gb EAA51559.1	hypothetical protein MG03154.4 [...	57	7e-07
gi 2114221 dbj BAA19990.1	phosphatase 2C motif [Homo sapiens]	57	8e-07
gi 18086420 gb AAL57666.1	AT5g53140/MFH8_8 [Arabidopsis th...	56	1e-06
gi 7661862 ref NP_055449.1	protein phosphatase 1F; partner...	56	1e-06
gi 20146110 dbj BAB88944.1	protein phosphatase 2C [Mesembr...	56	2e-06
gi 23506609 gb AAN37903.1	putative serine/threonine phosph...	56	2e-06
gi 228508 prf 1805227A	protein phosphatase 2C	55	2e-06

gi 25352221 pir T52337	phosphoprotein phosphatase (EC 3.1....	55	2e-06
gi 15230495 ref NP_190715.1	protein phosphatase 2C (PP2C),...	55	2e-06
gi 6320198 ref NP_010278.1	serine-threonine protein phosph...	55	2e-06
gi 2137765 pir I49016	phosphoprotein phosphatase (EC 3.1.3...	55	3e-06
gi 6319415 ref NP_009497.1	protein phosphatase type 2C; Pt...	55	3e-06
gi 2137695 pir S65672	phosphoprotein phosphatase (EC 3.1.3...	55	3e-06
gi 33859600 ref NP_035281.1	protein phosphatase 1B, magnes...	55	3e-06
gi 27806079 ref NP_776855.1	protein phosphatase 1B (former...	55	3e-06
gi 18423476 ref NP_568786.1	protein phosphatase 2C (PP2C),...	55	3e-06
gi 30684431 ref NP_188351.2	protein phosphatase 2C (PP2C) ...	55	4e-06
gi 25144464 ref NP_741087.1	protein phosphatase type-2C (5...	54	4e-06
gi 12666519 emb CAC28024.1	protein phosphatase 1B2 53 kDa ...	54	4e-06
gi 16416087 emb CAB91227.2	related to Type 2C Protein Phos...	54	5e-06
gi 15081703 gb AAK82506.1	Atlg78200/T11I11_14 [Arabidopsis...	54	5e-06
gi 32415453 ref XP_328206.1	Type 2C Protein Phosphatase re...	54	5e-06
gi 4505995 ref NP_002697.1	protein phosphatase 1B isoform ...	54	5e-06
gi 16223994 gb AAL15579.1	hFEM-2 [Homo sapiens]	54	9e-06
gi 20978304 gb AAM33411.1	putative protein phosphatase PP2...	53	1e-05
gi 11282002 pir T47644	protein phosphatase 2C-like protein...	53	1e-05
gi 546853 gb AAB30830.1	Tpdlp=protein phosphatase 2C homol...	53	2e-05
gi 18416366 ref NP_568237.1	protein phosphatase 2C (PP2C) ...	52	2e-05

Alignments

>gi|39573724|ref|NP_945149.1| protein phosphatase 2C eta isoform 2; protein phosphatase 2C eta

[Mus musculus]

gi|37704769|gb|AAR01612.1| protein phosphatase 2C eta [Mus musculus]

Length = 406

Score = 704 bits (1816), Expect = 0.0

Identities = 345/387 (89%), Positives = 366/387 (94%), Gaps = 3/387 (0%)

Query: 76 IINA EKSEFNEDQAACGKLCIRRC EFGAEE--EWLTLCPEEFLTGHYWALFDGHGGPAAA 133

+INA EKSEFNEDQAACGKLCIRRC EFG EE EWLT+CPEEFLTGHYWALFDGHGGPAAA

Sbjct: 20 VINA EKSEFNEDQAACGKLCIRRC EFGIEEDQEWLTVCP EEF LTGHYWALFDGHGGPAAA 79

Query: 134 ILAANTLH SCLRRQLEAVVEGLVATQPPMHLN GRCICPSDPQFVEEKGIRAEDLVIGALE 193

ILAANTLH SCLRRQLEAVVEG++A QPPMHL+GRC+CPSDPQFVEEKGI+AEDLVIGALE

Sbjct: 80 ILAANTLH SCLRRQLEAVVEGMMAPQPPMHL SGRVCVCPSDPQFVEEKGIQAEDLVIGALE 139

Query: 194 SAFQECDEVIGRELEASGQMG GCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEF 253

+AFQECD+VIGRELEASGQ+GGCTALVAV LQGKLY+ANAGDSRAILVRR EIR LS EF

Sbjct: 140 NAFQECDDVIGRELEASGQVG GCTALVAVFLQGKLYVANAGDSRAILVRRHEIRQLSSEF 199

Query: 254 TPETERQRIQQ LAFVYPELLAGEFTRLEFP RRLKGDDL GQKVLFRDHHMSGWSYKRVEKS 313

TPETERQRIQQ LAF YPELLAGEFTRLEFP RRLKGDDL GQKVLFRDHHM GWSYKRVEKS

Sbjct: 200 TPETERQRIQQ LAF TYP ELLAGEFTRLEFP RRLKGDDL GQKVLFRDHHMRGWSYKRVEKS 259

Query: 314 DLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TN IQLKPFLLSVPQVTVLVDV DQLEL 373

DLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD T+IQLKPFLLS+PQVTVLDV QL +

Sbjct: 260 DLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TDIQLKPFLLSIPQVTVLVDVHQLAV 319

Query: 374 QEDDVVVMATDGLWDVLSNEQVAWLVR SFLPGNQ-EDPHRF SKLAQM LIHSTQGKEDSLT 432

QE+DVVVMATDGLWDVLSNEQVA LVR SFL GNQ +DPHRF S+LA+MLIH+TQGK++ T

Sbjct: 320 QEEDVVVMATDGLWDVLSNEQVALLVR SFLTGNQKDDPHRF SELAKMLIHNTQGKDN GAT 379

Query: 433 EEGQVSYDDVSVFVIPLHSQGQESSDH 459
 EGQVSYDDVSVFVIPLHSQ QE S H
 Sbjct: 380 GEGQVSYDDVSVFVIPLHSQAQEGSGH 406

>gi|26338027|dbj|BAC32699.1| unnamed protein product [Mus musculus]
 gi|26378394|dbj|BAB28679.2| unnamed protein product [Mus musculus]
 gi|34849561|gb|AAH58248.1| RIKEN cDNA 2810423O19 [Mus musculus]
 Length = 306

Score = 544 bits (1402), Expect = e-153
 Identities = 269/306 (87%), Positives = 288/306 (94%), Gaps = 1/306 (0%)

Query: 155 LVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGALESASFQECDEVIGRELEASGQMG 214
 ++A QPPMHL+GRC+CPSDPQFVEEKGI+AEDLVIGALE+AFQECD+VIGRELEASGQ+G
 Sbjct: 1 MIAPQPPMHLSGRCVCPSDPQFVEEKGIQAEDLVIGALENAFQECDDVIGRELEASGQVG 60

Query: 215 GCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQALAFVYPELLA 274
 GCTALVAV LQGKLY+ANAGDSRAILVRR EIR LS EFTPETERQRIQQALAF YPELLA
 Sbjct: 61 GCTALVAVFLQGKLYVANAGDSRAILVRRHEIRQLSSEFTPETERQRIQQALAFVYPELLA 120

Query: 275 GEFTRLEFPRLKGGDLGQKVLFRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLA 334
 GEFTRLEFPRLKGGDLGQKVLFRDHMM GWSYKRVEKSDLKYPLIHGQGRQARLLGTLA
 Sbjct: 121 GEFTRLEFPRLKGGDLGQKVLFRDHMRGWSYKRVEKSDLKYPLIHGQGRQARLLGTLA 180

Query: 335 VSRGLGDHQLRVLDTNQLKPFLLSVPQVTVLVDVQLELQEDDVVVMATDGLWDVLSNEQ 394
 VSRGLGDHQLRVLDLT+IQLKPFLLS+PQVTVLDV QL +QE+DVVVMATDGLWDVLSNEQ
 Sbjct: 181 VSRGLGDHQLRVLDTDIQLKPFLLSIPQVTVLDVHQLAVQEEDVVVMATDGLWDVLSNEQ 240

Query: 395 VAWLVRSFLPGNQ-EDPHRFSLAQMMLIHSTQGKEDSLTEEGQVSYDDVSVFVIPLHSQG 453
 VA LVRSFL GNQ +DPHRS+LA+MLIH+TQGK++ T EGQVSYDDVSVFVIPLHSQ
 Sbjct: 241 VALLVRSFLTGNQKDDPHRFSELAQMMLIHNTQGKDNGATGEGQVSYDDVSVFVIPLHSQA 300

Query: 454 QESSDH 459
 QE S H
 Sbjct: 301 QEGSGH 306

>gi|21389471|ref|NP_653242.1| hypothetical protein FLJ32332 [Homo sapiens]
 gi|16552416|dbj|BAB71302.1| unnamed protein product [Homo sapiens]
 Length = 270

Score = 512 bits (1318), Expect = e-144
 Identities = 251/252 (99%), Positives = 252/252 (100%)

Query: 162 MHLNGRCICPSDPQFVEEKGIRAEDLVIGALESASFQECDEVIGRELEASGQMGGCTALVA 221
 MHLNGRCICPSDPQFVEEKGIRAEDLVIGALESASFQECDEVIGRELEASGQMGGCTALVA
 Sbjct: 1 MHLNGRCICPSDPQFVEEKGIRAEDLVIGALESASFQECDEVIGRELEASGQMGGCTALVA 60

Query: 222 VSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQALAFVYPELLAGEFTRLE 281
 VSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQALAFVYPELLAGEFTRLE
 Sbjct: 61 VSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQALAFVYPELLAGEFTRLE 120

Query: 282 FPRRLKGGDLGQKVLFRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGT LAVSRGLGD 341

FPRRLKGDDLQKQVLF RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGD
 Sbjct: 121 FPRRLKGDDLQKQVLF RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGD 180
 Query: 342 HQLRVLD TN IQLKPFLLSVPQVT VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWL VRS 401
 HQLRVLD TN IQLKPFLLSVPQVT VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWL VRS
 Sbjct: 181 HQLRVLD TN IQLKPFLLSVPQVT VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWL VRS 240
 Query: 402 FLPGNQEDPHRF 413
 FLPGNQEDPHR+
 Sbjct: 241 FLPGNQEDPHRY 252

>gi|16307111|gb|AAH09644.1| FLJ32332 protein [Homo sapiens]
 Length = 247

Score = 499 bits (1286), Expect = e-140
 Identities = 247/247 (100%), Positives = 247/247 (100%)

Query: 213 MGGCTALVAVSLQ GKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQ LAFVYPEL 272
 MGGCTALVAVSLQ GKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQ LAFVYPEL
 Sbjct: 1 MGGCTALVAVSLQ GKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQ LAFVYPEL 60
 Query: 273 LAGEFTRLEFPRRLKGDDLQ KQVLF RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGT 332
 LAGEFTRLEFPRRLKGDDLQ KQVLF RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGT
 Sbjct: 61 LAGEFTRLEFPRRLKGDDLQ KQVLF RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGT 120
 Query: 333 LAVSRGLGDHQLRVLD TN IQLKPFLLSVPQVT VLDVDQLELQEDDVVVMATDGLWDVLSN 392
 LAVSRGLGDHQLRVLD TN IQLKPFLLSVPQVT VLDVDQLELQEDDVVVMATDGLWDVLSN
 Sbjct: 121 LAVSRGLGDHQLRVLD TN IQLKPFLLSVPQVT VLDVDQLELQEDDVVVMATDGLWDVLSN 180
 Query: 393 EQVAWL VRSFLPGNQEDPHRF SKLAQM LIHSTQGKEDSLTEEGQVS YDDVS VFVIPLHSQ 452
 EQVAWL VRSFLPGNQEDPHRF SKLAQM LIHSTQGKEDSLTEEGQVS YDDVS VFVIPLHSQ
 Sbjct: 181 EQVAWL VRSFLPGNQEDPHRF SKLAQM LIHSTQGKEDSLTEEGQVS YDDVS VFVIPLHSQ 240
 Query: 453 GQESSDH 459
 GQESSDH
 Sbjct: 241 GQESSDH 247

>gi|12856386|dbj|BAB30649.1| unnamed protein product [Mus musculus]
 Length = 254

Score = 445 bits (1145), Expect = e-124
 Identities = 223/254 (87%), Positives = 235/254 (92%), Gaps = 1/254 (0%)

Query: 207 LEASGQMGGCTALVAVSLQ GKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQ L 266
 LEA GQ+GGCTALVAV LQGKLY+ANAGDSRAILVRR EIR LS EFTPETERQRIQQ L
 Sbjct: 1 LEALGQVGGCTALVAVFLQ GKLYVANAGDSRAILVRRHEIRQLSSEFTPETERQRIQQ L 60
 Query: 267 FVYPELLAGEFTRLEFPRRLKGDDLQ KQVLF RDHHMSGWSYKRVEKSDLKYPLIHGQGRQ 326
 F YPELLAGE TRLEFPRRLKGDDLQ KQVLF RDHHM GWSYKRVEKSDLKYPLIHGQGRQ
 Sbjct: 61 FTYPELLAGELTRLEFPRRLKGDDLQ KQVLF RDHHMRGWSYKRVEKSDLKYPLIHGQGRQ 120
 Query: 327 ARLLGTLAVSRGLGDHQLRVLD TN IQLKPFLLSVPQVT VLDVDQLELQEDDVVVMATDGL 386
 ARLLGTLAVSRGLGDHQLRVLD TN IQLKPFLLS+PQVT VLDV QL +QE+DVVVMATDGL

Sbjct: 121 ARLLGTLAVSRGLGDHQLRVLDTDIQLKPFLLSIPQVTVLDVHQLAVQEEDVVVMATDGL 180

Query: 387 WDVLSNEQVAWLVRSEFLPGNQ-EDPHRFSKLAQMLIHSTQGKEDSLTEEGQVSYDDVSVF 445
WDVLSNEQVA LVRSEFL GNQ +DPHRFS+LA+MLIH+TQGK++ T EGQVSYDDVSVF

Sbjct: 181 WDVLSNEQVALLVRSEFLTGNQKDDPHRFSKLAQMLIHNTQGKDNGATGEGQVSYDDVSVF 240

Query: 446 VIPLHSQGQESSDH 459

VIPLHSQ QE S H

Sbjct: 241 VIPLHSQAQEGSGH 254

>gi|28892713|ref|NP_795893.1| RIKEN cDNA A430075L18 gene [Mus musculus]

gi|26333637|dbj|BAC30536.1| unnamed protein product [Mus musculus]

Length = 469

Score = 357 bits (917), Expect = 2e-97

Identities = 206/433 (47%), Positives = 266/433 (61%), Gaps = 49/433 (11%)

Query: 30 PYRRPRFLRGSSSSPGAADASRRPDSRPVRSPARGRTL PWNAGYAEIINA EKSEFNEDQA 89
PY RP FL S + S +RP+ R LPW GYAE+INA KS NEDQA

Sbjct: 40 PYGRPEFL---GLSQDEVECSADHIARPILILKETRRLPWATGYAEVINAGKSTHNEDQA 96

Query: 90 ACGKLCIR-----RCEFGAEEEWLTL---CPEEFLTGHY WALFDGHGGPA 131
+C L ++ R E L L E ++ HYW+LFDGH G

Sbjct: 97 SCEVLTVKKKAGTITSTPNRNSKRRSSLPNGEGLQLKENSESEGISCHYWSLFDGHAGSG 156

Query: 132 AAAILAANTLHSCLRRLQLEAVVEGL--VATQPPMHL-----NGRCIC----- 170
AA++A+ L + +QL+ +VE L A PP L +GR +

Sbjct: 157 AAVVASRLQLHHITQQQLQDIVEILKNSAILPPTCLGEEPESTPAHGRTLTRAASLRGGVG 216

Query: 171 ----PSDP--QFVEEKGIRAEDLVIGALES AFQECDEVIGRELEASGMGGCTALVAVSL 224
PS P +F EK I E LVIGALES AF+E D I RE A GGCTAL+ V L

Sbjct: 217 APGSPSTPPTTRFFTEKKIPHECLVIGALES AFKEMDLQIERERSAYNISGGCTALIVVCL 276

Query: 225 QGKLYMANAGDSRAILVRRDEIRPLSF EFTPETERQRIQQ LAFVYPELLAGEFTRLEFPR 284
GKLY+ANAGDSRAI++R EI P+S EFTPETERQR+Q LAF+ P LL EFT LEFPR

Sbjct: 277 LGKLYVANAGDSRAIIRNGEIIIPMSSEFTPETERQRLQYLA FMQPHLLGNEFTHLEFPR 336

Query: 285 RLKGDDLQKQVLF RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQL 344
R++ +LG+K+L+RD +M+GW+YK +E DLK+PLI+G+G++AR++ T+ V+RGLGDH L

Sbjct: 337 RVQRKELGKKMLYRDFNMTGWAYKTIEDDDLKFPLIYGEGKKARVMATIGVTRGLGDHDL 396

Query: 345 RVLDTNIQLKPFLLSVPQVTVLDVDQLQEDDVVVMATDGLWDVLSNEQVAWLVRSEFLP 404
+V D+NI +KPFL S P+V V D+ + E DDV+++ATDGLWDVLSNE+VA + FLP

Sbjct: 397 KVHDSNIYIKPFLSSAPEVRVYDL SRYEHGADDVLILATDGLWDVLSNEEVAEAITQFLP 456

Query: 405 G-NQEDPHRFSKL 416

+ +DPHRF L

Sbjct: 457 NCDPDDPHRFVPL 469

>gi|29611652|ref|NP_082258.1| protein phosphatase 2a, catalytic subunit,
zeta isoform [Mus

musculus]

gi|29373411|gb|AAO72079.1| protein phosphatase 2C zeta [Mus musculus]

Length = 507

Score = 335 bits (858), Expect = 1e-90

Identities = 203/469 (43%), Positives = 274/469 (58%), Gaps = 33/469 (7%)

Query: 12 PGEPLPAPRPPGPHASVPYRRPRFLRGSSSSPGAADASRRPD--SRPVRSPA-RGRTL 68
 PG + AP+ + V + RP FL+ SPG R D R V+SP GR LP
 Sbjct: 49 PGNQVGAPQ---KTATVSFSRPTFLQ---LSPGGETLRRADDHAGRAVQSPDTRRLP 101

Query: 69 WNAGYAEIINA EKSEFNEDQAACGKLCIR----RCEFGAEEEWLTLCP EEF LTGHYWALF 124
 W+ GYAE+INA KS NEDQA C + + R G E + +YW LF
 Sbjct: 102 WSTGYAEVINAGKSRHNEDQACCEVVYVESRRSRSVTGV SRE---PSHNQGF CFYYWGLF 158

Query: 125 DGHGGPAAAILAANTLH SCLRRQLEAVVEGL----VATQPPMHLNGR C ICPSDPQFVE-- 178
 DGH G AA +A+ LH +R QL+ +VE L G PS Q V
 Sbjct: 159 DGHAGGGAAEMASRL LHRHIREQLKDLVEILK DPLPPPLCLPSTPGTPGAPSPSQLVSPQ 218

Query: 179 -----EKGIRAEDLVIGALES AFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANA 233
 +K + + L++GA+E+AF DE + RE GGC ALV + L GK+Y+ANA
 Sbjct: 219 SCWSPQKEVTHDSLIVGA IENAFHLMDEQMARERRGHQVEGGCCALVVL YLLGKMYVANA 278

Query: 234 GDSRAILVRRDEIRPLSFEFTPETERQRIQQLAFVYPELLAGEFTRLEFP RRLKGDDL GQ 293
 GDSRAI+VR EI P+S EFTPETERQR+Q L F+ PELL EFT LEFPRR++ +LGQ
 Sbjct: 279 GDSRAIIVRNGEII PMSREFTPETERQRLQLLGFLKPELLGSEFTHLEFPRRVQPKELGQ 338

Query: 294 KVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGLTAVSRGLGDHQLRVLD TN IQL 353
 ++L+RD +M+GW+YK++E DL++PL+ G+G++AR++ T+ V+RGLGDH L+V + + +
 Sbjct: 339 RMLYRDQNM TGWAYKKIEVEDLRFLVC GEGKKARVMATIGVTRGLGDHNLKVCSS T LSI 398

Query: 354 KPFLLSVPQVTVLDVDQLELQEDDVVMATDGLWDVLSNEQVAWLVR SFLPGNQ-EDPHR 412
 KPFL P+V V D+ Q E DDV+V+ TDGLWDV ++ +VA V L + DP R
 Sbjct: 399 KPFLSCFPEVRVYDLTQYEHCPDDVLVLGTDGLWDVTNDSEVAATVDRVLSSYEPNDPSR 458

Query: 413 FSKLAQMLIHSTQG----KEDSLTEEGQVS YDDVSVFVIPLHSQGQESS 457
 ++ LAQ L+ +G + L S DD+SVFVIPL G S
 Sbjct: 459 YTALAQALVLGARGIPRDRGWRLPNNKLGSGDDISVFVIPLGGPGSSYS 507

>gi|33873319|gb|AAH11803.2| MGC19531 protein [Homo sapiens]

Length = 488

Score = 334 bits (857), Expect = 2e-90

Identities = 202/452 (44%), Positives = 269/452 (59%), Gaps = 39/452 (8%)

Query: 31 YRRPRFLRGSSSSPGAADASRRPDSRPVRSPA-RGRTL PWNAGYAEIINA EKSEFNEDQA 89
 + RP FL+ SPG + R V+SP GR LPW+ GYAE+INA KS NEDQA
 Sbjct: 50 FSRPTFLQ---LSPGGLRRADDHAGRAVQSPDTRRLPWSTGYAEVINAGKSRHNEDQA 106

Query: 90 ACGKLCI--RRCEFGAEEEWLTLCP E--EFLTGHYWALFDGHGGPAAAILAANTLH SCLR 145
 C + + RR G E P + L +YW LFDGH G AA +A+ LH +R
 Sbjct: 107 CCEVVYVEGRRSVTGVPRE-----PSRGQGLCFYYWGLFDGHAGGGAAEMASRL LHRHIR 161

Query: 146 RQLEAVVE-----GLVATQPPMHLNGR C ICPSDPQFVEEKGIRAEDLVI 189
 QL+ +VE G + P HL G C S +K + E LV+
 Sbjct: 162 EQLKDLVEILQDPSPPPPLCLPTTPGTPDSSDSPHLLGPQSCWS-----SQKEVSHESLVV 216

Query: 190 GALESFAFQECDEVIGRELEASQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPL 249
 GA+E+AFQ DE + RE GGC ALV + L GK+Y+ANAGDSRAI+VR EI P+
 Sbjct: 217 GAIENAFQLMDEQMARERRGHQVEGGCCALVVIYLLGKVYVANAGDSRAIIVRNGEIIPM 276

Query: 250 SFEFTPETERQRIQQALAFVYPELLAGEFTRLEFPRLKGGDDLQKQVLFDRDHMSGWSYKR 309
 S EFTPETERQR+Q L F+ PELL EFT LEFPRR+ +LGQ++L+RD +M+GW+YK+
 Sbjct: 277 SREFTPETERQRLQLLGLFLKPELLGSEFTHLEFPRLVLPKELGQRMVLYRDQNMGTWAYKK 336

Query: 310 VEKSDLKYPLIHGQGRQARLLGLTAVSRGLGDHQLRVLDTNQLKPFLLSVPQVTVLDVD 369
 +E DL++PL+ G+G++AR++ T+ V+RGLGDH L+V + + +KPFL P+V V D+
 Sbjct: 337 IELEDLRFPLVLCGEGKKARVMATIGVTRGLGDHSLKVCSSSTLPKPFLLSCFPEVRVYDLT 396

Query: 370 QLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPH-RFSKLAQMLIHSTQGKE 428
 Q E DDV+V+ TDGLWDV ++ +VA V L + + H R++ LAQ L+ +G
 Sbjct: 397 QYEHCPDDVLVLGTDGLWDVTTDCEVAATVDRVLSAYEPNDHSRYTALAQALVLGARGTP 456

Query: 429 DS----LTEEGQVSYYDDVSFVIPLHSQGQES 456
 L S DD+SVFVIPL G S
 Sbjct: 457 RDRGWRLPNNKLGSGDDISVFVIPLGGPGSYS 488

>gi|31127152|gb|AAH52910.1| Unknown (protein for IMAGE:30075932) [Mus musculus]

Length = 424

Score = 332 bits (850), Expect = 1e-89

Identities = 182/368 (49%), Positives = 245/368 (66%), Gaps = 32/368 (8%)

Query: 114 EFLTGHYWALFDGHGGPAAAILAANTLHSCLRRLQLEAVVEGL--VATQPPMHL----- 164
 E ++ HYW+LFDGH G AA++A+ L + +QL+ +VE L A PP L
 Sbjct: 50 EGISCHYWSLFDGHAGSGAAVVASRLQHPITQQLQDIVEILKNSAILPPTCLGEEPEST 109

Query: 165 --NGRCIC-----PSDP--QFVEEKGIRAEDLVIGALESFAFQECDEVIGRE 206
 +GR + PS P +F EK I E LVIGALESFA+E D I RE
 Sbjct: 110 PAHGRTLTRAASLRGGVGAPGSPSTPPTTRFFTEKKIPHECLVIGALESFAFKEMDLQIERE 169

Query: 207 LEASQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQLA 266
 A GGCTAL+ V L GKLY+ANAGDSRAI++R EI P+S EFTPETERQR+Q LA
 Sbjct: 170 RSAYNISGGCTALIVVCLLGKLYVANAGDSRAIIRNGEIIPMSSEFTPETERQRLQYLA 229

Query: 267 FVYPELLAGEFTRLEFPRLKGGDDLQKQVLFDRDHMSGWSYKRVEKSDLKYPLIHGQGRQ 326
 F+ P LL EFT LEFPRR++ +LG+K+L+RD +M+GW+YK +E DLK+PLI+G+G++
 Sbjct: 230 FMQPHLLGNEFTHLEFPRLVQRKELGKKMLYRDFNMTGWAYKTIEDDDLKFPLIYGEGKK 289

Query: 327 ARLLGLTAVSRGLGDHQLRVLDTNQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGL 386
 AR++ T+ V+RGLGDH L+V D+NI +KPFL S P+V V D+ + E DDV+++ATDGL
 Sbjct: 290 ARVMATIGVTRGLGDHDLKVHDSNIYIKPFLSSAPEVRVYDLSRYEHGADDVLILATDGL 349

Query: 387 WDVLSNEQVAWLVRSLPG-NQEDPHRFSKLAQMLIHSTQG----KEDSLTEEGQVSYYDD 441
 WDVLSNE+VA + FL + +DPHR++ AQ L+ +G + ++ + S DD
 Sbjct: 350 WDVLSNEEVAEAITQFLNCDPDDPHRYTLAAQDLVMRARGVLKDRGWRISNDRLGSGDD 409

Query: 442 VSVFVIPL 449
 +SV+VIPL
 Sbjct: 410 ISVYVIPL 417

>gi|34859725|ref|XP_215663.2| similar to protein phosphatase 2C zeta
[Rattus norvegicus]

Length = 530

Score = 327 bits (838), Expect = 3e-88

Identities = 203/491 (41%), Positives = 278/491 (56%), Gaps = 56/491 (11%)

Query: 13 GEPLPAPRPPGPHASPVYRRPRFLRGSSSSPGAADASRRPDSRPVRSFA-RGRTL PWNA 71
G +PAP+ +PV + RP FL+ SPG + R V+SP GR LPW+
Sbjct: 50 GNEIPAPQKTA--ETPVFSRPTFLQ---LSPGGLRRADDHVGRAVQSPPDTGRRLPWST 104

Query: 72 GYAEIINA EKSEFNEDQAACGKLCI--RRCEFGAEEEWLTLCP EEF LTGHY WALFDGHGG 129
GYAE+INA KS NEDQA C + + RR G E + + +YW LFDGH G
Sbjct: 105 GYAEVINAGKSRHNEDQACCEVVYVESRRSITGVSRE---PSHNQGF SFYYWGLFDGHAG 161

Query: 130 PAAAILAANTLHSLRRQLEAVVEGL-----VATQPPMHLNGRCICPSDPQFV 177
AA +A+ LH +R QL+ +VE L P + + + P +
Sbjct: 162 GGAAEMASRLLRHIREQLKDLVEILQDPLPPPLCLPSTPGTPGVSSPSQLVSPQ--SWS 219

Query: 178 EEKGIRAEDLVIGALES AFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDS- 236
+K + + LV+GA+E+AFQ DE + RE GGC ALV V L GK+Y+ANAGDS
Sbjct: 220 PQKEVTHDSL VVGAIENAFQLMDEQMARERRGHLVEGGCCALVVVYLLGKMYVANAGDSS 279

Query: 237 -----RAILVRRDEIRPLSF EFTPETERQRIQQ LAFVYPE 271
RAI+VR EI P+S EFTPETERQR+Q L F+ PE
Sbjct: 280 PPAWNSPLCMNFSEKARSKSFLSLGRAIIVRNGEII PMSREFTPETERQRLQLLGFLKPE 339

Query: 272 LLAGEFTRLEFP RRLKGDDL GQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLG 331
LL EFT LEFPRR++ +LGQ++L+RD +M+GW+YK++E DL++PL+ G+G++AR++
Sbjct: 340 LLGSEFTHLEFP RRVQPKELGQRM L YRDQNM TGWAYKKIELEDLRFPLVCGE GK KARVMA 399

Query: 332 TLAVSRGLGDHQLRVLD TN IQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLS 391
T+ V+RGLGDH L+V + + +KPFL P+V V D+ Q E DDV+V+ TDGLWDV +
Sbjct: 400 TIGVTRGLGDHNLKVCSS TLPIKPFLLSCFP EVRVYDLTQYEHCPDDVLVLGTDGLWDVTN 459

Query: 392 NEQVAWLVR SF LPGNQ-EDPHRF SKLAQM LIHSTQG----KEDSLTEEGQVS YDDVS VFV 446
+ +VA V L + DP R++ LAQ L+ +G + L S DD+SVFV
Sbjct: 460 DSEVAATVDRVLSTYEPNDPSRYTALAQA LVLGARGIPRDRGWRLPNNKLGSGDDISVFV 519

Query: 447 IPLHSQGQESS 457
IPL G S
Sbjct: 520 IPLGGPGSSYS 530

>gi|34526234|dbj|BAC85206.1| unnamed protein product [Homo sapiens]
Length = 169

Score = 311 bits (796), Expect = 2e-83

Identities = 155/156 (99%), Positives = 155/156 (99%)

Query: 304 GWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TN IQLKPFLLSVPQV 363
G SYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TN IQLKPFLLSVPQV
Sbjct: 14 GRSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TN IQLKPFLLSVPQV 73

Query: 364 TVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPHRFSKLAQMLIHS 423
 TVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPHRFSKLAQMLIHS
 Sbjct: 74 TVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPHRFSKLAQMLIHS 133

Query: 424 TQ GKEDSLTEEGQVS YDDVSVFVIPLHSQQQESSDH 459
 TQ GKEDSLTEEGQVS YDDVSVFVIPLHSQQQESSDH
 Sbjct: 134 TQ GKEDSLTEEGQVS YDDVSVFVIPLHSQQQESSDH 169

>gi|39930533|ref|NP_005158.4| hypothetical protein MGC19531 [Homo sapiens]
 gi|11360166|pir||T43442 hypothetical protein DKFZp434P1514.1 - human
 gi|6599183|emb|CAB63764.1| hypothetical protein [Homo sapiens]
 Length = 299

Score = 271 bits (692), Expect = 3e-71
 Identities = 141/287 (49%), Positives = 192/287 (66%), Gaps = 5/287 (1%)

Query: 175 QFVEEKGIRAEDLVIGALES AFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAG 234
 Q + K + E LV+GA+E+AFQ DE + RE GGC ALV + L GK+Y+ANAG
 Sbjct: 13 QLKDLKEVSHESLVVGA IENAFQLMDEQMARERRGHQVEGGCCALVVIYLLGKVYVANAG 72

Query: 235 DSRAILVRRDEIRPLSF EFTPETERQRIQQ LAFVYPELLAGEFTRLEFP RR LKGDDLQ GK 294
 DSR AI+VR EI P+S EFTPETERQR+Q L F+ PELL EFT LEFP RR+ +LGQ+
 Sbjct: 73 DSR AIIVRNGE IIPMSREFTPETERQRLQLLGFLKPELLGSEFTHLEFP RRVL PKELGQR 132

Query: 295 VLFRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGLTAVSRGLGDHQLRVLD TN IQLK 354
 +L+RD +M+GW+YK++E DL++PL+ G+G++AR++ T+ V+RGLGDH L+V + + +K
 Sbjct: 133 MLYRDQNM TGWAYKKIELEDLRFPLVCGEGKKARVMATIGVTRGLGDHSLKVCSS TLPIK 192

Query: 355 PFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPH-RF 413
 PFL P+V V D+ Q E DDV+V+ TDGLWDV ++ +VA V L + + H R+
 Sbjct: 193 PFLSCFP EVRVYDLTQYEHCPDDVLVLGTDGLWDVTTDCEVAATVDRVLSAYEPNDHSRY 252

Query: 414 SKLAQMLIHSTQ GKEDS-----LTEEGQVS YDDVSVFVIPLHSQQQES 456
 + LAQ L+ +G L S DD+SVFVIPL G S
 Sbjct: 253 TALAQA LVLGARGTPRDRGWRLPNNKLGSGDDISVFVIPLGGPGSYS 299

>gi|17539110|ref|NP_502329.1| protein phosphatase 2C-like (4N30)
 [Caenorhabditis elegans]
 gi|7497315|pir||T32903 hypothetical protein C42C1.2 - Caenorhabditis
 elegans
 gi|2804429|gb|AAB97544.1| Hypothetical protein C42C1.2 [Caenorhabditis
 elegans]
 Length = 582

Score = 261 bits (666), Expect = 2e-68
 Identities = 178/509 (34%), Positives = 261/509 (51%), Gaps = 93/509 (18%)

Query: 30 PYRRPRFLRGSSSSPG-AADASRRPDSRPVRSPARGRTL PWNAGYAEIINA EKSEFNEDQ 88
 PY RP FL S ++D S RP P R P R +P GYAE INA K+ NEDQ
 Sbjct: 56 PYSRPEFLYFSEEEIALSSDHSVRPVLCP-RFP HR---MPLYVG YAEAINAGKT VQ NEDQ 111

Query: 89 AACGKLCIRRCE-----FGAEEE-----WLTLCPEEF 115
 A+ L + + + F ++E+ +L + E+

Sbjct: 112 ASAKMLVLTQHQNEMNGFSSDEKKSETRKRNSNENDDDPMLTPGGDDTVSYLNVVNEKS 171

Query: 116 -----LTGHYWALFDGHGGPAAAILAANTLHSCLRRLQLEAVVEGLVATQPPMHLN---- 165
 G ++LFDGH G A A++A+ LH ++ +L V++ ++ +LN

Sbjct: 172 SMFAPRADGALFSLFDGHAGSAVAVVASKCLHEHVKSRLCEVLDTILHMDRHNENLNFNGKH 231

Query: 166 --GRCICPSDPQFVEEKGIRAEDLVIGALESFAFQECDEVIGRELEASGQMGGCTALVAVS 223
 S+ +E IR+E LV GALE+AF + DE I ++ + GGC + +

Sbjct: 232 RSESSYSMSEMSREDENRIRSEHLVKGALETAFLDMDEQIAQDKQVWRLPGGCAVISVLV 291

Query: 224 LQGKLY-----MANAGDSRAILVRRDEIRPL 249
 GKLY ++NAGD RAILV D R L

Sbjct: 292 FLGKLYIGGDFKNFFELSEGCHITIFPNSINVEKINNTRKLSNAGDCRAILVTSDGSRAL 351

Query: 250 SFEEFTPETERQRIQQLAFVYPELLAGEFTRLEFPRLKGGDLGQKVLFRDHHMSGWSYKR 309
 S + TP +ER+R+Q+LA+ PEL+ F+RLE+ +RL DL +VL+RD M GW+ K

Sbjct: 352 SKDLTPASERKRLQELAYRNPELIGNSFSRLEYSKRLTIHDLKSRVLYRDWFMWGAVVKT 411

Query: 310 VEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDLTNIQLKPFLLSVPQVTVLVDV- 368
 V++ DL+ LI R+ RLL T+ VSRG GDH L +D + +KPFL +VP+++V ++

Sbjct: 412 VKECDLRPSLISETSRKKRLNTIGVSRGFGDHHLLTVDERLSIKPFLLSAVPEISVTNLR 471

Query: 369 DQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSL- PGNQEDPHRFSLKLAQMLIHSTQGK 427
 D L + DVV++A+DGLWDVLSNE +VRS L + DP R+++ AQ L+ + +G+

Sbjct: 472 DMNTLTDKDVVIVASDGLWDVLSNEDAGLIVRSTLGSTDSADPSRYTQAAQDLVAAARGQ 531

Query: 428 EDS-----LTEEGQVSYDDVSVFVIPL 449
 + S + G SYDD++VFVIPL

Sbjct: 532 QASGNLKRWVMNTGGHASYDDITVFVIPL 560

>gi|31203861|ref|XP_310879.1| ENSANGP00000008051 [Anopheles gambiae]
 gi|30177994|gb|EAA06421.2| ENSANGP00000008051 [Anopheles gambiae str.
 PEST]

Length = 429

Score = 256 bits (654), Expect = 6e-67

Identities = 161/439 (36%), Positives = 243/439 (55%), Gaps = 36/439 (8%)

Query: 31 YRRPRFLRGSSSSPGAADASRRPDSRPVRSRARGRTL PWNAGYAEIINA EKSEFNEDQAA 90
 Y RP FL+ + A A + RP+ P LPW+ GYAE +N+ KS++NEDQAA

Sbjct: 6 YARPPFLQLLTYDELKASADH--NVRPIIVPRDISLLPWSTGYAECVNSGKSKWNEDQAA 63

Query: 91 CGKLCIRRCEFGAEEEWLTLCP EEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRLQLEA 150
 + + + L Y+ ++DGH G AA+ AAN H L +L

Sbjct: 64 FHRQVLSHPSRQYHD-----LPYTYFGIYDGHAGYGAALAAANQFHYILHEKLVD 113

Query: 151 VVEGLVATQPPMHLNG-----RCICPSDPQFVEEKGIRAEDLVIGALESFAFQECDEVIGR 205
 V++ L+ P + +G P F K + ++L++GALE+AF + D V+

Sbjct: 114 VIDLLM---PRVEGDGGGLALHATLPHPSLF--HKQVSKDELIVGALEAAAFADMDAVLAE 168

Query: 206 ELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEEFTPETERQRIQQL 265
 + + GGCTALVA+ + GKL++ANAGDSR +L +R P SF+ TP+TER R+ +

Sbjct: 169 DRDKYRNAGGCTALVALFILGKLFVANAGDSRGVLCKRVVAEPCSFDPDTERSLLTV 228

Query: 266 AFVYPELLAGEFTRLEFPRLKGGDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGR 325

P LL GE+ +E+ ++ DLG ++L+R M GW+YK + +DLK PLI G G+

Sbjct: 229 GKHNPLLGGEYIAMEYAKKPTTKDLGARILYRQGAMKGWYKTLTATDLKIPLITGVGK 288

Query: 326 QARLLGTLAVSRGLGDHQLRVLDTNQLKPFLLSVPQVTVLDVDQLELQEDD----- 377
 ++RLLGT+ V+RG GDH L+ L +N+ +KPFL + P V D+ Q+ + D

Sbjct: 289 RSRLLTIGVTRGFGDHDHLKALGSNLPIKPFLSAHPDVVCFDLAQVRSEPADENS DGEYG 348

Query: 378 VVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPHRFSLAQMLIHSTQGKEDS-----L 431
 ++VMATDGLWDV ++QVA V L + HR++ +AQ L+ ++G+ +

Sbjct: 349 ILVMATDGLWDVSESQQVANTVFGTLKRFPARHRYTMVAQELVARSRGRANESGHWRLS 408

Query: 432 TEEGQVSYDDVSVFVIPLH 450
 + DD+SV VIP+H

Sbjct: 409 DSRAAATVDDISVIVIPVH 427

>gi|19920426|ref|NP_608468.1| CG17598-PA [Drosophila melanogaster]
 gi|17944215|gb|AAL48002.1| GM14138p [Drosophila melanogaster]
 gi|22832704|gb|AAF50944.2| CG17598-PA [Drosophila melanogaster]
 Length = 651

Score = 255 bits (651), Expect = 1e-66
 Identities = 165/467 (35%), Positives = 247/467 (52%), Gaps = 53/467 (11%)

Query: 24 PHASVPYRRPRFLRGSSSSPGAADASRRPDSRPVRSRPARGRTL PWNAGYAEIINA EKSE 83
 P PY RP FL+ +P AS + RP+ P LPW GYAE +N+ KSE

Sbjct: 52 PMPDKFPYARPPFLQ--LLTPDELASADHNVRPIIVPRDINLLPWGTGYAECVNSGKSE 109

Query: 84 FNEDQAACGKLCIRRCFEGAEEEWLTLCPEEFLTGHYWALFDGHGGPAAAAILAANTLHSC 143
 +NEDQ A + + E + L Y+ +FDGH G AA+ A++ H

Sbjct: 110 WNEDQGAFCRQVLSDEHKHPD-----LPYTYFGIFDGHAGYGAALAASHQFHFI 159

Query: 144 LRRQLEAVVEGLV---ATQPPMHLNGRCICPSDPQFVE-EKGIRAEDLVIGALES AFQEC 199
 L +L +E L+ A G + P+ P + ++ + ++L+IGALES AF

Sbjct: 160 LHEKLVDCLELLLPDADATNGGGEGNKLNPTFPHPPIYFQRRVTKDELIIGALES AFFNM 219

Query: 200 DEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRR----- 243
 D +I ++ + GGCTA V++ + GK+Y+ANAGDSRA+L +R

Sbjct: 220 DSLIAQDCDRYRDAGGCTACVSLFIDGKMYVANAGDSRAVLCQRRATPERPQTNTDSGIE 279

Query: 244 -DEIR-----PLSFETPETERQRIQQLAFVYPELLAGEFTRLEFPRLKGGDLGQKVL 296
 D + P S + TPETER+R+ +A + P L+ + +E+ +R D+GQ++L

Sbjct: 280 PDPLEASCYPVPFSADHTPETERERLLNVARLKPMLMGKHYVAMEYAKRPHIKDMGQRIL 339

Query: 297 FRDHHSMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKPF 356
 R M GW+YK + DL P+++G+G+++RLLGTL V+RG GDH+L ++T IQ+KPF

Sbjct: 340 CRQGTMRGWYKTLTMEDLCMPVVNGEGKRSRLGLGTVTRGFGDHELLAINTGIQIKPF 399

Query: 357 LLSVPQVTVLDVDQLELQEDD-----VVVMATDGLWDVLSNEQVAWLVRSLPGNQE 408
 L P V D+ Q+ D+ V+VMATDGLWDV N+ V+ V L

Sbjct: 400 LTPHPDVRQRDLTQVVSIPDEDNRDGDYGLVLMATDGLWDVSENDVSRVTFQTL SKYST 459

Query: 409 DPHRFSLAQMLIHSTQGK-EDS-----LTEEGQVSYDDVSVFVIPL 449
 + HR++ +AQ L+ +GK DS + + DD+SV VIP+

Sbjct: 460 EKHYTMVAQELVARARGKINDSGHWRLADSKAAATVDDISVIVIPV 506

>gi|3242077|emb|CAA05875.1| protein phosphatase 2C [Arabidopsis thaliana]
Length = 511

Score = 89.4 bits (220), Expect = 1e-16
Identities = 88/352 (25%), Positives = 153/352 (43%), Gaps = 96/352 (27%)

Query: 116 LTGHYWALFDGHGGPAAAILAANTLHSCLRRLQLEAVVEGLVATQPPMHLNGRCICPSDPQ 175
LTGH++ ++DGHGG A + LH L ++E + + L C +
Sbjct: 234 LTGHFFGVYDGHGGHKVADYCRDLRHFALAEIERIKDEL-----CKRNTG 279

Query: 176 FVEEKGIRAEDLVIGALESQECDEVIGRE-----LEA-SGQMGCTALVAVSLQG 226
E + ++ + + + E + IGR LEA + + G TA+VA+
Sbjct: 280 --EGRQVQWDKVFVTSCFLTVDGEIEGKIGRAVVGSSDKVLEAVASETVGSTAVVALVCSS 337

Query: 227 KLYMANAGDSRAILVRRDEIRPLSFEEFTPETERQRIQQALFVYPELLAGEFTRLEFPRL 286
+ ++N GDSRA+L R E PLS + P+ E E+ R+E
Sbjct: 338 HIVVSNCGDSRAVLFRGKEAMPLSVDHKPDRE-----DEYARIE----- 376

Query: 287 KGDDLQKQVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRV 346
+ G KV+ Q + AR+ G LA+SR +GD L
Sbjct: 377 ---NAGGKVI-----QWQGARVFGVLAMSRSIGDRYL-- 405

Query: 347 LDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR--FLP 404
KP+++ P+VT + +ED+ +++A+DGLWDV++N++V + R +
Sbjct: 406 -----KPYVIPEPEVTFMP----RSREDECLILASDGLWDMNNQVECEIARRRILMW 454

Query: 405 GNQEDPHRFKSLAQMLIHSTQGKEDSLT----EEGQVSYDDVSFVFIPLHSQ 452
+ ++ + + + Q D L+ ++G S D++S+ VI L +Q
Sbjct: 455 HKKNGAPPLAERGGIDPACQAAADYLSMLALQKG--SKDNISIIVIDLKAQ 504

>gi|7768151|emb|CAB90633.1| protein phpsphatase 2C (PP2C) [Fagus sylvatica]
Length = 413

Score = 88.2 bits (217), Expect = 3e-16
Identities = 94/373 (25%), Positives = 154/373 (41%), Gaps = 96/373 (25%)

Query: 94 LCIRRCEFGAEEEWLTLCPPEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRLQLEAVVE 153
+C RR E E+ +++ P H++ +FDGHG A+ + LH ++ ++E+V E
Sbjct: 126 VCGRRREM---EDAVSVHPSVSNNFHFVDFDGHGCSHVAMRCRDLHDIVKEEVESVTE 182

Query: 154 GLVATQPPMHLNGRCICPSDPQFVEEK-GIRAEDLVIGALESQECDEVIGRELEASGQ 212
G+ R D + E + I+ + + +CD V
Sbjct: 183 GMEWKDTMEKSFDRM----DKEVQEWVRVPIKTNC---RCDVQTPQCDAV----- 225

Query: 213 MGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEEFTPETERQRIQQALFVYPEL 272
G TA+VA+ K+ ++N GDSRA+L R PLS + P+ P+
Sbjct: 226 --GSTAVVAIVTPEKIIIVSNCGDSRAVLCRNGVAFPLSSDHKPDRE-----PD- 270

Query: 273 LAGEFTRLEFPRLKGGDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGT 332
E R++ D G +V++ D AR+LG
Sbjct: 271 ---ELVRIQ-----DAGGRVIYWD-----GARVLGV 293

Query: 333 LAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSN 392

LA+SR +GD+ L KP+++S P+VT+ D ED+ +++A+DGLWDV+SN
 Sbjct: 294 LAMSRAIGDNYL-----KPYVISEPEVTITD-----RTAEDECLILASDGLWDVVSN 340

Query: 393 EQVAWLVRSLPGNQEDPHRFSKLAQMLIHSTQGKEDSLTEEGQV-----SYDDV 442
 E + R L + S M + + D + + S D+V

Sbjct: 341 ETACGVARMCLRAQKPSSPPRSPGNDMAVGAAESSDKACSDASILLTKLALARHSTDNV 400

Query: 443 SVFVIPLHSQGQE 455
 SV V+ L Q+

Sbjct: 401 SVVVVDLRRNHQQ 413

>gi|30685388|ref|NP_173199.2| protein phosphatase 2C (PP2C) -related
 [Arabidopsis thaliana]
 Length = 511

Score = 88.2 bits (217), Expect = 3e-16
 Identities = 80/288 (27%), Positives = 131/288 (45%), Gaps = 73/288 (25%)

Query: 115 FLTGHYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDP 174
 +LT H++ ++DGHGG A + +HS L ++E + E L GR + +

Sbjct: 232 YLTSHFFGVYDGHGGAQVADYCHDRIHSALAEIEIERIKEELCRRNTG---EGRQV-QWEK 287

Query: 175 QFVEEKGIRAEDLVIGAL-ESAFQECDEVIGRELEA-SGQMGGCTALVAVSLQGKLYMAN 232
 FV+ ++ +D V G + D ++ LEA S + G TA+VA+ + ++N

Sbjct: 288 VFVDCY-LKVDDEVKGKINRPVVGSSDRMV---LEAVSPETVGSTAVVALVCSSHIIVSN 343

Query: 233 AGDSRAILVRRDEIRPLSFEEPTETERQRIQQALFVYPELLAGEFTRLEFPRLKGGDDL 292
 GDSRA+L+R + PLS + P+ E +

Sbjct: 344 CGDSRAVLLRGKDSMPLSVDHKPDREDE----- 371

Query: 293 QKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQ 352
 Y R+EK+ K +I QG AR+ G LA+SR +GD

Sbjct: 372 -----YARIEKAGGK--VIQWQG--ARVSGVLAMRSRIGDQ-----Y 404

Query: 353 LKPFLLSVPQVTVLVDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR 400
 L+PF++ P+VT + +ED+ +++A+DGLWDV+SN++ R

Sbjct: 405 LEFPFVIPDPEVTFMP----RAREDECLILASDGLWDVMSNQEACDFAR 448

>gi|26452332|dbj|BAC43252.1| unknown protein [Arabidopsis thaliana]
 Length = 511

Score = 88.2 bits (217), Expect = 3e-16
 Identities = 80/288 (27%), Positives = 131/288 (45%), Gaps = 73/288 (25%)

Query: 115 FLTGHYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDP 174
 +LT H++ ++DGHGG A + +HS L ++E + E L GR + +

Sbjct: 232 YLTSHFFGVYDGHGGAQVADYCHDRIHSALAEIEIERIKEELCRRNTG---EGRQV-QWEK 287

Query: 175 QFVEEKGIRAEDLVIGAL-ESAFQECDEVIGRELEA-SGQMGGCTALVAVSLQGKLYMAN 232
 FV+ ++ +D V G + D ++ LEA S + G TA+VA+ + ++N

Sbjct: 288 VFVDCY-LKVDDEVKGKINRPVVGSSDRMV---LEAVSPETVGSTAVVALVCSSHIIVSN 343

Query: 233 AGDSRAILVRRDEIRPLSFEEPTETERQRIQQALFVYPELLAGEFTRLEFPRLKGGDDL 292

GDSRA+L+R + PLS + P+ E +
 Sbjct: 344 CGDSRAVLLRGKDSMPLSVDHKPDREDE----- 371
 Query: 293 QKVLFRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQ 352
 Y R+EK+ K +I QG AR+ G LA+SR +GD
 Sbjct: 372 -----YARIEKAGGK--VIQWQG--ARVSGVLAMSRSIGDQ-----Y 404
 Query: 353 LKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR 400
 L+PF++ P+VT + +ED+ +++A+DGLWDV+SN++ R
 Sbjct: 405 LEFPFVIPDPEVTFMP----RAREDECLILASDGLWDVMSNQEACDFAR 448

>gi|33309516|gb|AAQ03211.1| protein phosphatase 2C [Prunus avium]
 Length = 426

Score = 85.9 bits (211), Expect = 2e-15
 Identities = 84/313 (26%), Positives = 134/313 (42%), Gaps = 81/313 (25%)

Query: 118 GHYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNRCICPSDPQFV 177
 H++ +FDGHG A+ + LH ++++LE G + + M R D + V
 Sbjct: 165 AHFYGVFDGHGCSHVALKCKDRLHEIVKQELETE--GGYIQWKGAME---RSFAKMDDE-V 219
 Query: 178 EEKGIRAE DLVIGALES AFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSR 237
 +E + A+ E +CD V G TA+VAV K+ ++N GDSR
 Sbjct: 220 QEGNLVAQGPNC-RCELQTPQCDAV-----GSTAVVAVVTPEKIIVSNCGDSR 266
 Query: 238 AILVRRDEIRPLSFETTPETERQRIQQALAFVYPELLAGEFTRLEFPRLKGGDDLQKVL F 297
 A+L R PLS + P+ P+ E R+E G +V++
 Sbjct: 267 AVLRCRNGVAVPLSSDHKPDR-----PD----ELVRIEAA-----GGRVIY 302
 Query: 298 RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFL 357
 D AR+LG LA+SR +GD+ L KP++
 Sbjct: 303 WD-----GARVLGVLAMSRAIGDNYL-----KPYV 327
 Query: 358 LSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR SFLPGNQEDPHRFSKLA 417
 +S P+VT++D ED+ +++A+DGLWDV+SN+ +VR L + H S
 Sbjct: 328 ISEPEVTIMD----RSAEDECLILASDGLWDVVSNDTACGVVRMCLRAQKTTSHSESSGR 383
 Query: 418 QMLIHSTQ GKEDS 430
 + S + D+
 Sbjct: 384 DAAVRSDKACSDA 396

>gi|21902025|dbj|BAC05575.1| protein phosphatase 2C-like protein [Oryza
 sativa (japonica
 cultivar-group)]
 Length = 467

Score = 81.3 bits (199), Expect = 3e-14
 Identities = 82/300 (27%), Positives = 125/300 (41%), Gaps = 95/300 (31%)

Query: 110 LCPEEF-LTGHYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNRC 168
 L P F L H++ ++DGHGG A LH+ L +L + +EG V+
 Sbjct: 189 LDPMSFRLPAHFFGVYDGHGGAQVANYCRERLHAALVEEL-SRIEGSVSG----- 237

Query: 169 ICPSDPQFVEEKGIRAEDLVIGALES AFQECDEVIGRELEASGQMG-----GCTALV 220
 ++ VE K E AF +C + E+ + G G TA+V
 Sbjct: 238 ---ANLGSVEFKK-----KWEQAFVDCFSRVDEEVGGNASRGEAVAPETVGSTAVV 285

Query: 221 AVSLQGKLYMANAGDSRAILVRRDEIRPLSF EFTPETERQRIQQ LAFVYPELLAGEFTRL 280
 AV + +AN GDSRA+L R + PLS + P E E+ R+
 Sbjct: 286 AVICSSHIIVANC GDSRAVLCRGKQP VPLSVDHKPNRE-----DEYARI 329

Query: 281 EFPRRLKGDDLQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLG 340
 E G KV+ Q R+ G LA+SR +G
 Sbjct: 330 EAE-----GGKVI-----QWNGYRVFGVLAMSR SIG 355

Query: 341 DHQLRVLD TN IQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR 400
 D L KP+++ VP++T++ ++D+ +V+A+DGLWDV+SNE+V + R
 Sbjct: 356 DRYL-----KPWIIPVPEITIVP----RAKDDECLVLASDGLWDVMSNEEVCDVAR 402

>gi|15222398|ref|NP_172223.1| protein phosphatase 2C (PP2C), putative
 [Arabidopsis thaliana]
 gi|25352229|pir|B86209 protein F22G5.22 [imported] - Arabidopsis thaliana
 gi|8778547|gb|AAF79555.1| F22G5.22 [Arabidopsis thaliana]
 gi|17979175|gb|AAL49783.1| putative protein phosphatase 2C [Arabidopsis
 thaliana]
 gi|20259129|gb|AAM14280.1| putative phosphatase 2C [Arabidopsis thaliana]
 Length = 442

Score = 80.1 bits (196), Expect = 7e-14

Identities = 82/287 (28%), Positives = 120/287 (41%), Gaps = 92/287 (32%)

Query: 119 HYWALFDGHGGPAAAILAANTLHSLRRQLEAVEGLVATQPPMHLNGRCICPSDPQFVE 178
 HY+ ++DGHG A LH + Q EA+ + + M R D + V
 Sbjct: 156 HYFGVYDGHGCSHVAARCKERLHEL V--QEEALSDKKEEWKKMME---RSFTRMDKEVV- 209

Query: 179 EKGIRAEDLVIGA---LES AFQECDEVIGRELEASGQMG GCTALVAVSLQGKLYMANAGD 235
 R + V+ A E +CD V G TA+V+V K+ +AN GD
 Sbjct: 210 ----RWGETVMSANCRCELQTPDCDAV-----GSTAVVSVITPEKIIVANC GD 253

Query: 236 SRAILVRRDEIRPLSF EFTP E--TERQRIQQ LAFVYPELLAGEFTRLEFPRLKGGDDLQ 293
 SRA+L R + PLS + P+ E RIQ+ G
 Sbjct: 254 SRAVLCRNGKAVPLSTDHKPDRPDELDR IQEA-----GG 287

Query: 294 KVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TN IQL 353
 +V++ D AR+LG LA+SR +GD+ L
 Sbjct: 288 RVIYWD-----GARVLGVLAMSRAIGDNYL----- 312

Query: 354 KPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR 400
 KP++ S P+VTV D +ED+ +++ATDGLWDV++NE +VR
 Sbjct: 313 KPYVTSEPEVTVTD----RTEEDEFLLILATDGLWDVVTNEAACTMVR 355

>gi|8778461|gb|AAF79469.1| F1L3.26 [Arabidopsis thaliana]
 Length = 656

Score = 79.3 bits (194), Expect = 1e-13

Identities = 80/310 (25%), Positives = 136/310 (43%), Gaps = 89/310 (28%)

Query: 115 FLTGHYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDP 174
 +LT H++ ++DGHGG A + +HS L ++E + E L GR + +
 Sbjct: 349 YLTSHFFGVYDGHGGAQVADYCHDRIHSALAEIERIKEELCRRNTG---EGRQV-QWEK 404

Query: 175 QFVEEKGIRAEDLVIGAL-ESAFQECDEVIGRELEA-SGQMGGCTALVAVSLQGKLYMAN 232
 FV+ ++ +D V G + D ++ LEA S + G TA+VA+ + ++N
 Sbjct: 405 VFVDCY-LKVDDEVKGINRPVVGSSDRMV---LEAVSPETVGSTAVVALVCSSHIIVSN 460

Query: 233 AGDSRAILVRRDEIRPLSFEFTPETERQRIQQALAFVYPELLAGEFTRLEFPRLKGDDL 292
 GDSRA+L+R + PLS + P+ E +
 Sbjct: 461 CGDSRAVLLRGKDSMPLSVDHKPDREDE----- 488

Query: 293 QKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDT--- 349
 Y R+EK+ K +I QG AR+ G LA+SR + ++R++ T
 Sbjct: 489 -----YARIEKAGGK--VIQWQG--ARVSGVLAMRSI---EMRIITTCYS 527

Query: 350 -----NIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVL 390
 + L+PF++ P+VT + +ED+ +++A+DGLWDV+
 Sbjct: 528 LCKIMRSPESGFSASFSGDQYLEPFVIPDPEVTFMP----RAREDECLILASDGLWDVM 583

Query: 391 SNEQVAWLVR 400
 SN++ R
 Sbjct: 584 SNQEACDFAR 593

>gi|3643082|gb|AAC36697.1| protein phosphatase-2C; PP2C [Mesembryanthemum
 crystallinum]
 Length = 380

Score = 78.6 bits (192), Expect = 2e-13
 Identities = 90/336 (26%), Positives = 143/336 (42%), Gaps = 98/336 (29%)

Query: 119 HYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVE 178
 H++ ++DGHGG A A +H + + EG+ A
 Sbjct: 134 HFFGVYDGHGGSQVAGFCAQRMHEIIAEENQ--EGIDAY----- 171

Query: 179 EKGIRAEDLVIGALESFAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRA 238
 E R ++ I S F+ D+ I E+ AS +M G TA+VAV ++ ++N GDSRA
 Sbjct: 172 EWQKRWKEAFI---SGFKRADDQITTEVIAS-EMVGSTAVVAVVSGCQIILSNCGDSRA 226

Query: 239 ILVRRDEIRPLSFEFTPETERQRIQQALAFVYPELLAGEFTRLEFPRLKGDDLQKVLFR 298
 +L RR + PL+ + P+ E ELL R++G G +V+
 Sbjct: 227 VLCRRRTQTIPLTVDHKPDRE-----DELL-----RIEQ--GGRVI-- 260

Query: 299 DHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKPFLL 358
 W+ AR+ G LA+SR +GD + PF++
 Sbjct: 261 -----NWN-----GARVFGVLAMSRAIGDRYM-----SPFII 287

Query: 359 SVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPHRFSLKLAQ 418
 VP+VT ED+ +++A+DGLWDV+SN++ + + R +
 Sbjct: 288 PVPEVTF----TTRSDEDECLILASDGLWDVISNDEAGEV-----ARRLLRRRRRAMVA 337

Query: 419 MLIHSTQGKEDSLTEE--GQVSYDDVSFVFIPLHSQ 452
 I Q D LT+ G+ S D++SV V+ L S+
 Sbjct: 338 GDICPAQVVADKLTQLAIGRNSSDNISVIVVDLKS 373

>gi|15229745|ref|NP_187748.1| protein phosphatase 2C (PP2C), putative
 [Arabidopsis thaliana]
 gi|1352681|sp|P49598|P2C4_ARATH Protein phosphatase 2C (PP2C)
 gi|1076391|pir||S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C -
 Arabidopsis thaliana
 gi|633028|dbj|BAA07287.1| protein phosphatase 2C [Arabidopsis thaliana]
 gi|12322910|gb|AAG51448.1| protein phosphatase 2C (PP2C); 28184-26716
 [Arabidopsis thaliana]
 gi|18389242|gb|AAL67064.1| putative protein phosphatase PP2C [Arabidopsis
 thaliana]
 gi|20259229|gb|AAM14330.1| putative protein phosphatase 2C (PP2C)
 [Arabidopsis thaliana]
 Length = 399

Score = 78.6 bits (192), Expect = 2e-13
 Identities = 81/296 (27%), Positives = 124/296 (41%), Gaps = 92/296 (31%)

Query: 119 HYWALFDGHGGPAAAILAANTLHSLRRQLEAV-----VEGLVATQPPMHLNGRCICPSD 173
 H++ +FDGHG A LH +++++E + E +V + M
 Sbjct: 136 HFYGVFDGHGCSHVAEKCRERLHDIVKKEVEVMASDEWTETMVKSFKQMD----- 185

Query: 174 PQFVEEKGIRAEDLVI-GALESAFQECD-EVIGRELEASGQMGGCTALVAVSLQGKLYMA 231
 +E R +LV+ GA S C E+ + +A G TA+V+V K+ ++
 Sbjct: 186 ----KEVSQRECNLVVNGATRSMKNSCRCELQSPQCDAVGS----TAVVSVVTPPEKIIVS 237

Query: 232 NAGDSRAILVRRDEIRPLSFEFTPE--TERQRIQQALAFVYPELLAGEFTRLEFPRLKGD 289
 N GDSRA+L R PLS + P+ E RIQQ
 Sbjct: 238 NCGDSRAVLRCRNGVAIPLSVDHKKPDRPDELIRIQQA----- 273

Query: 290 DLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD 349
 G +V++ D AR+LG LA+SR +GD+ L
 Sbjct: 274 --GGRVIYWD-----GARVLGVLAMSRAIGDNYL----- 300

Query: 350 NIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPG 405
 KP+++ P+VTV D ED+ +++A+DGLWDV+ NE + R L G
 Sbjct: 301 ----KPYVIPDPEVTVD----RTDEDECLILASDGLWDVVPNETACGVARMCLRG 348

>gi|609658|gb|AAA67321.1| protein phosphatase 2C (ptc3+)
 Length = 414

Score = 77.0 bits (188), Expect = 7e-13
 Identities = 84/341 (24%), Positives = 138/341 (40%), Gaps = 104/341 (30%)

Query: 120 YWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEE 179
 ++A++DGHGG A + L L + +P F +
 Sbjct: 57 FFAVYDGHGGDKVAKWCGSNLPQILEK-----NPDF--Q 88

Query: 180 KGIRAEDLVIGALESFQECDDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAI 239
 KG D V AL+S+F D+ I + + GCTA V + + KLY ANAGDSR +
 Sbjct: 89 KG----DFV-NALKSSFLNADKAILDDDDQFHTDPSGCTATVVLRVGNKLYCANAGDSRTV 143

Query: 240 LVRRDEIRPLSFEFTPETERQRIQQALAFVYPELLAGEFTRLEFPRLKGDLDGQKVLFRD 299

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      L + +PLS + P E ++ + A      AG F      D G
Sbjct: 144 LGSKGI AKPLSADHKPSNEAEKARICA-----AGGFV-----DFG----- 178

Query: 300 HHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKP---F 356
      R+ G LA+SR +GD +      TN L+P
Sbjct: 179 -----RVNGNLALSRAIGDFEF-----TNSNLEPEKQI 206

Query: 357 LLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAVLVRSFLPGNQEDPHRF SKL 416
      + ++P V V ++      +D+ VV+A DG+WD +++QV VR +      K+
Sbjct: 207 VTALPDVVVHEIT----DDDEFVVLACDGIWDCKTSQQVIEFVRRGIVAGTS-----LEKI 258

Query: 417 AQMLIHSTQ GKEDSLTEEGQVSYDDVSFVIPLHSQQQESS 457
      A+ L+ +      + TE + D+++V ++ L + +S+
Sbjct: 259 AENLMDNCIASD---TETTGLGCDNMTVCIVALLQENDKSA 296

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>gi|16226419|gb|AAL16163.1| AT5g59220/mnc17_110 [Arabidopsis thaliana]
      Length = 413

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      Score = 76.6 bits (187), Expect = 1e-12
      Identities = 79/289 (27%), Positives = 115/289 (39%), Gaps = 89/289 (30%)

```

```

Query: 119 HYWALFDGHGGPAAAILAANTLHSCLRRLQLEAVVEGLVATQPPMHLNGRCICPSDPQFVE 178
      HY ++DGHG      A+      LH +R + EA +      +      R      D + V
Sbjct: 147 HYCGVYDGHGCSHVAMKCRERLHELVRREEFEADADWEKSM-----ARSFTRMDMEVV- 198

Query: 179 EKGIRAEDLVIGALESASFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRA 238
      + A+      E      +CD V      G TA+V+V      K+ +AN GDSRA
Sbjct: 199 --ALNADGAAKCRCELQRPDCDAV-----GSTAVVSVLTPEKIIIVANC GDSRA 244

Query: 239 ILVRRDEIRPLSF EFTPE--TERQRIQQI LAFVYPELLAGEFTRLEFP RRLKGDDLQKVL 296
      +L R +      LS + P+      E RIQ      G +V+
Sbjct: 245 VLCRNGKAIALSSDHKPD RPDELDR IQAA-----GGRVI 278

Query: 297 FRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKPF 356
      + D      R+LG LA+SR +GD+ L      KP+
Sbjct: 279 YWD-----GPRVLGV LAMSRAIGDNYL-----KPY 303

Query: 357 LLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAVLVRSFLPG 405
      ++S P+VTV D      DD +++A+DGLWDV+SNE      +VR L G
Sbjct: 304 VISRPEVTVTD----RANGDDFLILASDGLWDVVSNETACSVVRMCLRG 348

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>gi|15237839|ref|NP_200730.1| protein phosphatase 2C (PP2C), putative
[Arabidopsis thaliana]
gi|9759243|dbj|BAB09767.1| contains similarity to Ca/calmodulin-dependent
protein kinase
      phosphatase~gene_id:MNC17.13 [Arabidopsis thaliana]
gi|15809792|gb|AAL06824.1| AT5g59220/mnc17_110 [Arabidopsis thaliana]
gi|18377817|gb|AAL67095.1| AT5g59220/mnc17_110 [Arabidopsis thaliana]
      Length = 413

```

```

      Score = 76.6 bits (187), Expect = 1e-12
      Identities = 79/289 (27%), Positives = 115/289 (39%), Gaps = 89/289 (30%)

```


Query: 119 HYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVE 178
 HY ++DGHG A+ LH +R + EA + + R D + V
 Sbjct: 147 HYCGVYDGHGCSHVAMKCRERLHELVEEFADADWEKSM-----ARSFTRMDMEVV- 198

Query: 179 EKGIRAEDLVIGALESFAFQECDEVIGRELEASQMGGCTALVAVSLQGKLYMANAGDSRA 238
 + A+ E +CD V G TA+V+V K+ +AN GDSRA
 Sbjct: 199 --ALNADGAAKCRCELQRPDCDAV-----GSTAVVSVLTPEKIIIVANCGDSRA 244

Query: 239 ILVRRDEIRPLSFEEFTPE--TERQRIQQALAFVYPELLAGEFTRLEFPRLKGGDLGQKVL 296
 +L R + LS + P+ E RIQ G +V+
 Sbjct: 245 VLCRNGKAIALSSDHKPDRLPDELDRIQAA-----GGRVI 278

Query: 297 FRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNILQKPF 356
 + D R+LG LA+SR +GD+ L KP+
 Sbjct: 279 YWD-----GPRVLGVLAMSRAIGDNYL-----KPY 303

Query: 357 LLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPG 405
 ++S P+VTV D DD +++A+DGLWDV+SNE +VR L G
 Sbjct: 304 VISRPEVTVTD----RANGDDFLILASDGLWDVVSNETACSVVRMCLRG 348

>gi|15236110|ref|NP_194338.1| protein phosphatase ABI1 [Arabidopsis thaliana]
 gi|21431817|sp|P49597|P2C1_ARATH Protein phosphatase 2C ABI1 (PP2C) (Absciscic acid-insensitive 1)
 gi|7488009|pir||T04263 phosphoprotein phosphatase (EC 3.1.3.16) ABI1 - Arabidopsis thaliana
 gi|499301|emb|CAA54383.1| ABI1 [Arabidopsis thaliana]
 gi|549981|gb|AAA50237.1| absciscic acid insensitive protein
 gi|4538937|emb|CAB39673.1| protein phosphatase ABI1 [Arabidopsis thaliana]
 gi|7269459|emb|CAB79463.1| protein phosphatase ABI1 [Arabidopsis thaliana]
 gi|23297060|gb|AAN13081.1| phosphatase ABI1 [Arabidopsis thaliana]
 Length = 434

Score = 76.3 bits (186), Expect = 1e-12

Identities = 73/284 (25%), Positives = 118/284 (41%), Gaps = 91/284 (32%)

Query: 118 GHYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFV 177
 H++ ++DGHGG A +H L + +A + PM +C D
 Sbjct: 170 AHFFGVYDGHGGSQVANYCRERMHLALAE-----IAKEKPM-----LCDGDTWLE 215

Query: 178 EEKGIRAEDLVIGALESFAFQECDEVIGRELEA-SGQMGGCTALVAVSLQGKLYMANAGDS 236
 + K AL ++F D E+E+ + + G T++VAV +++AN GDS
 Sbjct: 216 KWKK-----ALFNSFLRVDS----EIESVAPETVGSTSVVAVVFP SHIFVANCGDS 262

Query: 237 RAILVRRDEIRPLSFEEFTPETERQRIQQALAFVYPELLAGEFTRLEFPRLKGGDLGQKVL 296
 RA+L R PLS + P+ E E R+E G KV+
 Sbjct: 263 RAVLCRGKTALPLSVDHKPDRE-----DEAARIEAA-----GGKVI 298

Query: 297 FRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNILQKPF 356
 Q AR+ G LA+SR +GD L KP
 Sbjct: 299 -----QWNGARVFGVLAMSR SIGDRYL-----KPS 323

Query: 357 LLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR 400
 ++ P+VT + ++EDD +++A+DG+WDV+++E+ + R

Sbjct: 324 IIPDPEVTAVK----RVKEDDCLILASDGVWDVMTDEEACEMAR 363

>gi|509419|emb|CAA55484.1| ABI1 [Arabidopsis thaliana]
Length = 434

Score = 76.3 bits (186), Expect = 1e-12
Identities = 73/284 (25%), Positives = 118/284 (41%), Gaps = 91/284 (32%)

Query: 118 GHYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFV 177

H++ ++DGHGG A +H L + +A + PM +C D

Sbjct: 170 AHFFGVYDGHGGSQVANYCRERMHLALAE-----IAKEKPM-----LCDGDTWLE 215

Query: 178 EEKGIRAEDLVIGALESASFQECDEVIGRELEA-SGQMGGCTALVAVSLQGKLYMANAGDS 236

+ K AL ++F D E+E+ + + G T++VAV +++AN GDS

Sbjct: 216 KWKK-----ALFNSFLRVDS----EIESVAPETVGSTSVVAVVFPSHIFVANC GDS 262

Query: 237 RAILVRRDEIRPLSFEEFTPETERQRIQQLAFVYPELLAGEFTRLEFPRLKGDLDLQKVL 296

RA+L R PLS + P+ E E R+E G KV+

Sbjct: 263 RAVLCRGKTALPLSVDHKPDRE-----DEAARIEAA-----GGKVI 298

Query: 297 FRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGLTAVSRGLGDHQLRVLDTNILKPF 356

Q AR+ G LA+SR +GD L KP

Sbjct: 299 -----QWNGARVFGVLAMSRSIGDRYL-----KPS 323

Query: 357 LLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAVLVR 400

++ P+VT + ++EDD +++A+DG+WDV+++E+ + R

Sbjct: 324 IIPDPEVTAVK----RVKEDDCLILASDGVWDVMTDEEACEMAR 363

>gi|10432446|emb|CAC10358.1| protein phosphatase 2C [Nicotiana tabacum]
gi|22553023|emb|CAC84141.2| protein phosphatase 2C [Nicotiana tabacum]
Length = 416

Score = 76.3 bits (186), Expect = 1e-12
Identities = 84/346 (24%), Positives = 138/346 (39%), Gaps = 100/346 (28%)

Query: 119 HYWALFDGHGGPAAAILAANTLHSLRRQLEA--VVEGLVATQPPMHLNGRCICPSDPQF 176

H++ ++DGHG A+ + +H ++ ++E V TQ ++ + S

Sbjct: 152 HFYGVYDGHGCSHVAMKCKDRMHEIVKNEVEKGETQWKEVMTQSFSQMDNEVVHYSS--- 208

Query: 177 VEEKGIRAEDLVIGALESASFQECD-EVIGRELEASGQMGGCTALVAVSLQGKLYMANAGD 235

GAL + C E+ + +A G TA+VAV K+ ++N GD

Sbjct: 209 -----GALGGSRSNCRCELQTPQCDVGS----TAVVAVVTPEKIIVSNCGD 251

Query: 236 SRAILVRRDEIRPLSFEEFTPTE--TERQRIQQLAFVYPELLAGEFTRLEFPRLKGDLDLQ 293

SRA+L R PLS + P+ E RIQ+ G

Sbjct: 252 SRAVLCRNGVAIPLSIDHKPDRPDELNRIQEA-----GG 285

Query: 294 KVLFRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGLTAVSRGLGDHQLRVLDTNIL 353

+V++ D R+LG LA+SR +GD+ L

Sbjct: 286 RVIYWD-----GPRVLGVLAMSRAGDNYL----- 310

Query: 354 KPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAVLVRSLPGNQEDPHRF 413

KP+++S P+VT+ + +ED+ +++A+DGLWDV+SNE + R L +

Sbjct: 311 KPYVISEPEVTITE-----RTEEDECLILASDGLWDVVSNETACGVARMCLQSRKPPSPHG 366

Query: 414 SKLAQMLIHSTQKGEDSLTEEGQV-----SYDDVSVFVIPL 449
 S + + D L + + S D+VSV V+ L

Sbjct: 367 SPENDVTVTGAGESSDQLCSDASILLTKLALARHSTDNVSVVVVDL 412

>gi|14334800|gb|AAK59578.1| putative protein phosphatase ABI1 [Arabidopsis thaliana]

Length = 434

Score = 76.3 bits (186), Expect = 1e-12

Identities = 73/284 (25%), Positives = 118/284 (41%), Gaps = 91/284 (32%)

Query: 118 GHYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFV 177
 H++ ++DGHGG A +H L + +A + PM +C D

Sbjct: 170 AHFFGVYDGHGGSQVANYSRERMHLALAE-----IAKEKPM-----LCDGDTWLE 215

Query: 178 EEKGIRAEDLVIGALESASFQECDEVIGRELEA-SGQMGGCTALVAVSLQGKLYMANAGDS 236
 + K AL ++F D E+E+ + + G T++VAV +++AN GDS

Sbjct: 216 KWKK-----ALFNSFLRVDS-----EIESVAPETVGSTSVVAVVFPESHIFVANCGDS 262

Query: 237 RAILVRRDEIRPLSFEEFTPETERQRIQQALFVYPELLAGEFTRLEFPRLKGGDLGQKVL 296
 RA+L R PLS + P+ E E R+E G KV+

Sbjct: 263 RAVLCRGKTALPLSVDHKPDRE-----DEAARIEAA-----GGKVI 298

Query: 297 FRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKPF 356
 Q AR+ G LA+SR +GD L KP

Sbjct: 299 -----QWNGARVFGVLAMSRSIGDRYL-----KPS 323

Query: 357 LLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR 400
 ++ P+VT + ++EDD +++A+DG+WDV+++E+ + R

Sbjct: 324 IIPDPEVTAVK----RVKEDDCLILASDGVWDVMTDEEACEMAR 363

>gi|19113999|ref|NP_593087.1| protein phosphatase 2c homolog 3

[Schizosaccharomyces pombe]

gi|1171964|sp|Q09173|P2C3_SCHPO Protein phosphatase 2C homolog 3 (PP2C-3)

gi|2130393|pir||S62462 protein phosphatase 2c homolog 3 - fission yeast
 (Schizosaccharomyces pombe)

gi|1019405|emb|CAA91172.1| ptc3 [Schizosaccharomyces pombe]

Length = 414

Score = 75.9 bits (185), Expect = 1e-12

Identities = 82/339 (24%), Positives = 140/339 (41%), Gaps = 100/339 (29%)

Query: 120 YWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEE 179
 ++A++DGHGG A + L L + +P F +

Sbjct: 57 FFAVYDGHGGDKVAKWCGSNLPQILEK-----NPDF--Q 88

Query: 180 KGIRAEDLVIGALESASFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAI 239
 KG D V AL+S+F D+ I + + GCTA V + + KLY ANAGDSR +

Sbjct: 89 KG----DFV-NALKSSFLNADKAILDDDQFHTDPSGCTATVVLRVGNKLYCANAGDSRTV 143

Query: 240 LVRRDEIRPLSFEEFTPETERQRIQQALFVYPELLAGEFTRLEFPRLKGGDLGQKVLFRD 299

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      L + +PLS + P E ++ + A      AG F      D G
Sbjct: 144 LGSKGI AKPLSADHKPSNEAEKARICA-----AGGFV-----DFG----- 178

Query: 300 HHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGLTAVSRGLGDHQLRVLDTNIQ-LKPFL 358
      R+ G LA+SR +GD + + ++N++ K +
Sbjct: 179 -----RVNGNLALSRAIGDFEFK--NSNLEPEKQIVT 208

Query: 359 SVPQVTVLVDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPHRFSKLAQ 418
      ++P V V ++      +D+ VV+A DG+WD +++QV VR +      K+A+
Sbjct: 209 ALPDVVVHEIT----DDDEFVVLACDGIWDCKTSQQVIEFVRRGIVAGTS----LEKIAE 260

Query: 419 MLIHSTQGKEDSLTEEGQVSYDDVSVFVIPLHSQGQESS 457
      L+ + + TE + D+++V ++ L + +S+
Sbjct: 261 NLMDNCIASD---TETTGLGCDNMTVCIVALLQENDKSA 296

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>gi|15227078|ref|NP_180499.1| protein phosphatase 2C (PP2C), putative
[Arabidopsis thaliana]
gi|25352214|pir||F84695 probable protein phosphatase 2C [imported] -
Arabidopsis thaliana
gi|3980397|gb|AAC95200.1| putative protein phosphatase 2C [Arabidopsis
thaliana]
Length = 362

```

Score = 75.5 bits (184), Expect = 2e-12
Identities = 80/299 (26%), Positives = 123/299 (41%), Gaps = 90/299 (30%)

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Query: 119 HYWALFDGHGGPAAAILAANTLHSCLRRLQLEAVVEGLVATQPPMHLNGRCICPSDPQFVE 178
      HY+ ++DGHG A LH ++ +L + +E + M R D + V
Sbjct: 111 HYFGVYDGHGCSHVAARCRERLHKLVLQEESSDMEDEEEWKTTME---RSFTRMDKEVVS 167

Query: 179 EKGIRAEDLVIGALESASFQE--CDEVIGRELEASQMGGCTALVAVSLQGKLYMANAGDS 236
      + +V + Q CD V G TA+V+V K+ +AN GDS
Sbjct: 168 ----WGDSVVTANCKCDLQTPACDSV-----GSTAVVSVITPDKIVVANCGDS 211

Query: 237 RAILVRRDEIRPLSFETTPETERQRIQQALAFVYPELLAGEFTRLEFPRLKGDDLQKQVL 296
      RA+L R + PLS + P+ P+ E R+E G +V+
Sbjct: 212 RAVLCRNGKPVPLSTDHKPDR-----PD----ELDRIE-----GAGGRVI 247

Query: 297 FRDHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGLTAVSRGLGDHQLRVLDTNIQLKPF 356
      + D R+LG LA+SR +GD+ L KP+
Sbjct: 248 YWD-----CPRVLGVLAMSRAIGDNYL-----KPY 272

Query: 357 LLSVPQVTVLVDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPG-----NQEDP 410
      + P+VT+ D ++DD +++A+DGLWDV+SNE + R L G + EDP
Sbjct: 273 VSCEPEVTITD-----RRDDCLILASDGLWDVVSNETACSVARMCLRGGGRRQDNEDP 326

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>gi|38109901|gb|EAA55700.1| hypothetical protein MG01351.4 [Magnaporthe
grisea 70-15]
Length = 451

```

Score = 75.5 bits (184), Expect = 2e-12
Identities = 78/339 (23%), Positives = 137/339 (40%), Gaps = 119/339 (35%)

Query: 120 YWALFDGHGGPAAAILAANTLHSLRRQ-----LEAVVEGLVATQPPMHLNGRCICP 171
 ++ +FDGHGG A+ + + +H ++ Q +A+ +G +AT R I
 Sbjct: 63 FFGVFDGHGGDKVALFSGDNIHKIVQNQDTFKSGNYEQALKDGFATD-----RAIL- 114

Query: 172 SDPQFVEEKGIRAEDLVIGALESFAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMA 231
 +DP++ +E + GCTA V + K+Y+A
 Sbjct: 115 NDPKYEDE-----VSGCTACVGLLTDDKIYIA 141

Query: 232 NAGDSRAILVRRDEIRPLSFEFTPETERQRIQQALAFVYPELLAGEFTRLEFPRRLKGDDL 291
 NAGDSR++L + +PLSF+ P+ E ++ + A AG F D
 Sbjct: 142 NAGDSRSVLGVKGRAPLSFDHKPQNEGEKARITA-----AGGFV-----DF 183

Query: 292 GQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNI 351
 G R+ G LA+SR +GD + + +
 Sbjct: 184 G-----RVNGNLALSRAIGDFEFK---KSA 205

Query: 352 QLKP---FLLSVPQVTVLVDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQE 408
 +L P + + P V V D+ +D+ +V+A DG+WD S++ V VR + Q
 Sbjct: 206 ELAPEQQIVTAYPDVVVHDMG----DDDEFLVIACDGIWDCQSSQAVVEFVRRGIAAKQA 261

Query: 409 DPHRFSLKLAQMLIHSTQKGEDSLTEEGQVSYDDVSVFVI 447
 K+ + ++ + S +E G V D++++ +I
 Sbjct: 262 ----LEKICENMMDNCLA---SNSETGGVGCDNMTMIII 293

>gi|15242022|ref|NP_200515.1| protein phosphatase 2C, ABI2 [Arabidopsis thaliana]
 gi|3914239|sp|O04719|P2C2_ARATH Protein phosphatase 2C ABI2 (PP2C) (Abscisic acid-insensitive 2)
 gi|1945140|emb|CAA70163.1| ABI2 protein phosphatase 2C [Arabidopsis thaliana]
 gi|1945142|emb|CAA70162.1| ABI2 protein phosphatase 2C [Arabidopsis thaliana]
 gi|2564213|emb|CAA72538.1| ABI2 [Arabidopsis thaliana]
 gi|8777445|dbj|BAA97035.1| protein phosphatase 2C ABI2 (PP2C) [Arabidopsis thaliana]
 gi|22531154|gb|AAM97081.1| protein phosphatase 2C ABI2 [Arabidopsis thaliana]
 gi|31711886|gb|AAP68299.1| At5g57050 [Arabidopsis thaliana]
 Length = 423

Score = 74.7 bits (182), Expect = 3e-12
 Identities = 77/285 (27%), Positives = 121/285 (42%), Gaps = 87/285 (30%)

Query: 116 LTGHYWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSPDPQ 175
 L+ H++ ++DGHGG A + C R A+ E +V +P C D
 Sbjct: 156 LSAHFFGVYDGHGGSQVA-----NYCRERMHLALTEEIVKEKPEF-----CDGDTW 201

Query: 176 FVEEKGIRAEDLVIGALESFAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGD 235
 +EK +A L ++F D I + + + G T++VAV +++AN GD
 Sbjct: 202 --QEKWKKA-----LFNSFMRVDSEI-ETVAHAPETVGSTSVVAVVFPTHIFVANC GD 251

Query: 236 SRAILVRRDEIRPLSFEFTPETERQRIQQALAFVYPELLAGEFTRLEFPRRLKGDDLQGV 295
 SRA+L R LS + P+ + E R+E G KV
 Sbjct: 252 SRAVLRCRGKTPLALSVDHKPDRD-----DEAARIEAA-----GGKV 287

Query: 296 LFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKP 355
 + W+ AR+ G LA+SR +GD L KP
 Sbjct: 288 I-----RWN-----GARVFGVLAMSRSIGDRYL-----KP 312

Query: 356 FLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR 400
 ++ P+VT + ++EDD +++A+DGLWDV++NE+V L R
 Sbjct: 313 SVIPDPEVTSVR----RVKEDDCLILASDGLWDVMTNEEVCDLAR 353

>gi|32406686|ref|XP_323956.1| hypothetical protein [Neurospora crassa]
 gi|28920231|gb|EAA29607.1| hypothetical protein [Neurospora crassa]
 gi|28950040|emb|CAD70795.1| probable protein phosphatase 2C [Neurospora crassa]

Length = 439

Score = 74.7 bits (182), Expect = 3e-12
 Identities = 78/339 (23%), Positives = 137/339 (40%), Gaps = 119/339 (35%)

Query: 120 YWALFDGHGGPAAAILAANTLHSLRRQ-----LEAVVEGLVATQPPMHLNGRCICP 171
 ++ +FDGHGG A+ A +H + +Q +A+ +G +AT R I

Sbjct: 63 FFGVFDGHGGDKVALFAGANIHDIIAQDFTKGTGNYEQALKDGFATD-----RAIL- 114

Query: 172 SDPQFVEEKGIRAEDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMA 231
 +DP++ EE + GCTA V + K+++A

Sbjct: 115 NDPKYEEE-----VSGCTACVGLITDEKIFVA 141

Query: 232 NAGDSRAILVRRDEIRPLSFEFTPETERQRIQQLAFVYPELLAGEFTRLEFPRLKGGDDL 291
 NAGDSR++L + +PLSF+ P+ E ++ + A AG F D

Sbjct: 142 NAGDSRSVLGVKGRAPLSFDHKPQNEGEKARITA-----AGGFV-----DF 183

Query: 292 GQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTN 351
 G R+ G LA+SR +GD + + +

Sbjct: 184 G-----RVNGNLALSRAIGDFEFK---KSA 205

Query: 352 QLKP---FLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQE 408
 +L P + + P V V D+ +D+ +V+A DG+WD S++ V VR + Q+

Sbjct: 206 ELAPEQQIVTAYPDVMVHDL----ADDDEFVLVACDGIWDCQSSQAVVEFVRRGIAAKQD 261

Query: 409 DPHRFSKLAQMLIHSTQGKEDSLTEEGQVSYDDVSVFVI 447

K+ + ++ + S +E G V D++++ ++

Sbjct: 262 ----LDKICENMMDNCLA---SNSETGGVGCDNMTMIIV 293

>gi|25352225|pir||F86206 hypothetical protein [imported] - Arabidopsis thaliana

gi|8954030|gb|AAF82204.1| Contains similarity to protein phosphatase 2C from Arabidopsis

thaliana gb|AF085279. It contains a protein phosphatase 2C domain PF|00481

Length = 405

Score = 74.7 bits (182), Expect = 4e-12
 Identities = 98/426 (23%), Positives = 165/426 (38%), Gaps = 112/426 (26%)

Query: 39 GSSSSPGAADASRRPDSRPVRSFARGRTLFWNAGYAEIINAEKSEFNEDQAACGKLCIRR 98

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      GS S PG+      +RP + +      G   P +   A+      E      +      C R
Sbjct: 73  GSDSGPGSILKRKRPTTLDIPVAPVGIAAPISN--ADTPREESRAVEREGDGYSVYCKRG 130

Query: 99  CEFGAEEEEWLTLC-----PEEFLTGHYWALFDGHGGPAAAILAANTLHSLRRQL----- 148
      E+ + +      P++ + G      ++DGHGGP AA  AA  L S +  ++
Sbjct: 131  KREAMEDRFSAITNLQGDPKQAIFG----VYDGHGGPTAAEFAAKNLCSNILGEIVGGRN 186

Query: 149  -----EAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGALESASFQECDEVI 203
      EAV  G +AT      D +F++EK ++
Sbjct: 187  ESKIEEAVKRGYLAT-----DSEFLKEKNVK----- 212

Query: 204  GRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTTPETERQRIQ 263
      GG   + A+      G L +ANAGD RA+L      L+ +  P  + +R
Sbjct: 213  -----GGSCCVTALISDGNLVVANAGDCRAVL SVGGFAEALTS DHRPSRDDR-- 260

Query: 264  QLAFVYPELLAGEFTRLEFPRLKGGDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQ 323
      R+E  R+      L ++V  R +H      Y  +      L+  +
Sbjct: 261  -----NRIESSVRI----LAKEVTVRFYH----DYMVLITILQGGYVDTF 298

Query: 324  GRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMAT 383
      R+ G+LAVSRG+GD      LK +++S P++ +L ++      + + +++A+
Sbjct: 299  NSVWRIQGS LAVSRGIGD-----AHLKQWIISEPEINILRINP----QHEFLILAS 345

Query: 384  DGLWDVLSNEQVAWLVRSF L PGNQEDPHRFSKLAQMLIHSTQ GKEDSLTEEGQVS YDDVS 443
      DGLWD +SN++      + R F  G  +      +++      D      G  S DD+S
Sbjct: 346  DGLWDKVS NQEAVDIARPFCKGTDQKRKPLLACKKLV-----DLSVSRG--SLDDIS 395

Query: 444  VFVIPL 449
      V +I L
Sbjct: 396  VMLIQL 401

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>gi|17555234|ref|NP_497949.1| protein phosphatase 2C, possibly N-
myristoylated (39.1 kD) (3F743)
      [Caenorhabditis elegans]
gi|18266883|sp|P49596|P2C2_CAEEEL Probable protein phosphatase 2C T23F11.1
(P2C2)
gi|7508306|pir||T25181 hypothetical protein T23F11.1 - Caenorhabditis
elegans
gi|5824637|emb|CAA86456.2| Hypothetical protein T23F11.1 [Caenorhabditis
elegans]

```

Length = 356

Score = 74.3 bits (181), Expect = 4e-12

Identities = 76/295 (25%), Positives = 115/295 (38%), Gaps = 97/295 (32%)

```

Query: 120  YWALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEE 179
      ++A++DGHGG      + +      LH  +  Q E
Sbjct: 54  FFAVYDGHGGSKVSQYSGINLHKKVVAQKEF----- 84

Query: 180  KGIRAEDLVIGALESASFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAI 239
      +E  +  A+E  F E D+ +  + E      + G TA+V +  +G +Y  NAGDSRA+
Sbjct: 85  ----SEGNMKEAIEKGFLLEDQQMRVDEETKDDVSGTTAVVVLIKEGDVYCGNAGDSRAV 140

Query: 240  LVRRDEIRPLSFEFTP--ETERQRIQQLAFVYPELLAGEFTRLEFPRLKGGDLGQKVL 297
      E RPLSF+  P  ETE +RI      + AG

```

Sbjct: 141 SSVVGEARPLSFDHKPSHETEARRI-----IAAG----- 169

Query: 298 RDHHMSGW-SYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKPF 356
 GW + RV G LA+SR LGD + DT +

Sbjct: 170 -----GWVEFN RVN-----GNLALSRLGDFAFKNC DTKPAEEQI 204

Query: 357 LLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPH 411
 + + P V D+L + + +V+A DG+WDV++N++V VR L + DP

Sbjct: 205 VTAFPDVI---TDKLT-PDHEFIVLACDGIWDVMTNQEVVDFVREKL-AEK RDPQ 254

>gi|4336436|gb|AAD17805.1| protein phosphatase type 2C [Lotus japonicus]
 Length = 282

Score = 71.2 bits (173), Expect = 4e-11
 Identities = 79/269 (29%), Positives = 111/269 (41%), Gaps = 94/269 (34%)

Query: 189 IGALES AFQECDEVIGRELEASGQMG--GCTALVAVSLQ-GKLYMANAGDSRAILVRRDE 245
 + A++ A+ + D I LE SG++G G TA+ A+ + KL +AN GDSRA+L + E

Sbjct: 101 VEAVKKAYVDT DSTI---LEKSGELGRGGSTAVTAILINCQKL VVANLGDSRAVLCKNGE 157

Query: 246 IRPLSF EFTPETERQRIQQ LAFVYPELLAGEFTRLEFPRLKGDDLQKVLFRDHHMSGW 305
 PLS + P TE + I+ R F GD

Sbjct: 158 AIPLSVDHEPATESEDIRN-----RGGFVS NFPGD----- 187

Query: 306 SYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKPFLLSVPQVTV 365
 P + GQ LAVSR GD LK L S P VTV

Sbjct: 188 -----VPRVDGQ-----LAVSRAFGDK-----SLKKHLSSEPHVTV 218

Query: 366 LDVDQLELQEDDV--VVMATDGLWDVLSNEQVAWLVRSLPGNQEDPHRFSKLAQMLIHS 423
 EL +DD +++A+DGLW V+SN++ +R N +D +K

Sbjct: 219 -----ELIDDDAEFIILASDGLWKVMSNQEA VDAIR-----NVKDARSAAK----- 259

Query: 424 TQ GKEDSLTEEG--QVS YDDVS VFVIPLH 450
 +LTEE + S DD+S V+ L

Sbjct: 260 -----NLTEEALKRNSSDDISCVVRLQ 282

>gi|32492311|emb|CAE03844.1| OSJNBb0089K06.2 [Oryza sativa (japonica
 cultivar-group)]
 Length = 484

Score = 70.1 bits (170), Expect = 9e-11
 Identities = 99/374 (26%), Positives = 151/374 (40%), Gaps = 51/374 (13%)

Query: 39 GSSSSPGAADASRRPDSRPVRSPARGRTL PWNAGYAEIINA EKSEFNEDQAACGKLCIRR 98
 G SS+ GAA +RR P+ S A W + + A + ED + R

Sbjct: 85 GCSSTAGAA--ARR---LPLPSGASTAAAVWPVAFG SVSLAGRMRDMEDAVSL-----R 133

Query: 99 CEFGAEEEEWLTLCPEEF LTGHYWALFDGHGGPAAAAILAANTLHSC LRRQLEAVVEGLVAT 158
 F WL P H++A+FDGHGGP + L +H + ++ A L

Sbjct: 134 PSFCT---WLDGSPM-----HFFAVFDGHGGPHVSALCREQM HVIVAEEMVAEAAAALRQR 185

Query: 159 QPPMHLNGR C ICPSDPQFVEEK GIRAEDLVIGALES AFQECDEVIGRELEASGQMG---G 215
 QP V E G SGQ G G

Sbjct: 186 QPAAMEEEEEERAVAGGAVAE-----LRPGGRAGGGGVRVRARHRAGVPCPLSGQTGAIIG 241

Query: 216 CTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEEFTPETERQRIQQQLAFVYPELLAG 275
 TA+VA+ ++ +L ++N GDSRA+L R + PLS + L+

Sbjct: 242 STAVVALLVRDRLVVSNCGDSRAVLCRAGDPLPLSSDHKGLNPS-----LSW 288

Query: 276 EFTRLEFPRLKGGDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQA-----RLL 330
 TR+ R GD GQ V +SG ++ ++ D K + GR R+

Sbjct: 289 RGTRVALARGTWGDKTGQSVGPAALLSSGGAHP--DRPDEKARIEAVGGRVVYLNGPRVR 346

Query: 331 GTLAVSRGLGD-HQLRVLDTNQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDV 389
 G LA+SR L + L + LKP ++ P +T+ + +D+ +++A+DG+WDV

Sbjct: 347 GILAMSRALAEGSSLLGPKGDKYLKPEVICEPDITI----TVRTVDDECLILASDGMWDV 402

Query: 390 LSNEQVAWLVRSL 403
 +SNE + + R L

Sbjct: 403 ISNETASDVARQCL 416

>gi|39591591|emb|CAE71168.1| Hypothetical protein CBG18025 [Caenorhabditis briggsae]

Length = 352

Score = 69.3 bits (168), Expect = 1e-10

Identities = 63/224 (28%), Positives = 94/224 (41%), Gaps = 64/224 (28%)

Query: 191 ALESAFQECDEVIGRELEASGQMGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLS 250
 A+E F + D+ + + E + G TA+V + +G +Y NAGDSRA+ E RPLS

Sbjct: 92 AIERGFLDLDDQMRVDEETKDDVSGTTAVVVLKEGDVYCGNAGDSRAVSSVLGEARPLS 151

Query: 251 FEFTP--ETERQRIQQQLAFVYPELLAGEFTRLEFPRLKGGDLGQKVLFRDHHMSGW-SY 307
 F+ P E E +RI + AG GW +

Sbjct: 152 FDHKPSHEIEARRI-----IAAG-----GWVEF 174

Query: 308 KRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKPFLLSVPQVTVLD 367
 RV G LA+SR LGD + DT + + + P V

Sbjct: 175 NRVN-----GNLALSRLGDFTFKNCDTKPAEEQIVTAFDPDVI--- 212

Query: 368 VDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPH 411
 D+L + + +V+A DG+WDV++N++V VR L + DP

Sbjct: 213 TDKLT-PDHEFIVLACDGIWDVMTNQEVVDFVREKL-SEKRDPQ 254

>gi|6478146|emb|CAB61839.1| putative serine/threonine phosphatase type 2c [Sporobolus

stapfianus]

Length = 271

Score = 69.3 bits (168), Expect = 1e-10

Identities = 82/338 (24%), Positives = 136/338 (40%), Gaps = 121/338 (35%)

Query: 121 WALFDGHGGPAAAILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEK 180
 + +FDGHGG AA AA + P+FV E+

Sbjct: 44 FGVFDGHGGKNAAEFAAENM-----PKFVAEE 70

Query: 181 GIRA---EDLVIGALESFAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSR 237
 +A E + GA++ + + DE E G+ GG + AV +G L ++N GD R
 Sbjct: 71 MTKADGGGESEIEGAVKRGYLKTDE----EFLRRGESGGACCVTAVLQKGLLVVSNVGD CR 126

Query: 238 AILVRRDEIRPLSF EF--TPETERQRIQQLAFVYPELLAGEFTRLEFPRLKGGDDLQKQV 295
 A+L R + L+ + + E E++RI+ +LG V
 Sbjct: 127 AVLSRSGKAEALTS DHRASREDEKERIE-----NLGGFV 160

Query: 296 LFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGLTAVSRGLGDHQLRVLD TN IQLKP 355
 + ++ W R+ G+LAVSRG+GD LK
 Sbjct: 161 V---NYRGTW-----RVQGS LAVSRGIGD-----AHLKQ 186

Query: 356 FLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR SFLPGNQEDPHRFSK 415
 ++++ P L VDQ + +++A+DGLWD + N++ L R N + S+
 Sbjct: 187 WIVADPDTRTLLVDQ---HCEFLILASDGLWDKIDNQEAVDLARPLCTSND----KASR 238

Query: 416 LA--QMLIHSTQ GKEDSLTEEGQVSYDDVSVFVIPLHS 451
 +A +ML+ ++ + S DD+SV +I L +
 Sbjct: 239 MAACRMLVETSI SRG-----STDDISVVIIQLQN 267

>gi|15220548|ref|NP_176948.1| protein phosphatase 2C (PP2C), putative
 [Arabidopsis thaliana]
 gi|25404969|pir||H96700 protein F12A21.5 [imported] - Arabidopsis thaliana
 gi|11072032|gb|AAG28911.1| F12A21.5 [Arabidopsis thaliana]
 Length = 464

Score = 68.6 bits (166), Expect = 2e-10
 Identities = 69/286 (24%), Positives = 118/286 (41%), Gaps = 90/286 (31%)

Query: 120 YWALFDGHGGPAAAAILAANTLHSC LRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEE 179
 ++ ++DGHGG AA A LH + +E C + VE
 Sbjct: 151 FFGVYDGHGGAKAAEFVAENLHKYV VEMMEN-----CKGKEEKVE- 190

Query: 180 KGIRAEDLVIGALESFAFQEC D----EVIGRELEASGQMGGCTALVAVSLQGKLYMANAGD 235
 A ++AF D E + +E G + G + AV ++ ++N GD
 Sbjct: 191 -----AFKAAFLRTDRDFLEKVIKEQSLKGVVSGACCVTAVIQDQEMIVSNLGD 239

Query: 236 SRAILVRRDEIRPLSF EFTP--ETERQRIQQLAFVYPELLAGEFTRLEFPRLKGGDDLQ 293
 RA+L R L+ + P + E++RI+ + + P + G L+G
 Sbjct: 240 CRAVLCRAGVAEALTD D HKPGRDDEKERIESQSLI-PFMTFG-----LQGG---- 284

Query: 294 KVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGLTAVSRGLGDHQLRVLD TN IQL 353
 + D+H W R+ G LAVSR +GD L
 Sbjct: 285 ---YVDNHQGA W-----RVQGILAVSR SIGD-----AHL 310

Query: 354 KPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWL V 399
 K ++++ P+ VL+++Q + + +V+A+DGLWDV+SN++ + V
 Sbjct: 311 KKVVVAEPETRVLELEQ---DMEFLVLASDGLWDVVS NQEAVYTV 352

>gi|34908256|ref|NP_915475.1| putative protein phosphatase 2C [Oryza sativa
 (japonica
 cultivar-group)]

gi|20160622|dbj|BAB89568.1| putative protein phosphatase 2C [Oryza sativa
(japonica
cultivar-group)]
Length = 405

Score = 67.8 bits (164), Expect = 4e-10
Identities = 95/382 (24%), Positives = 151/382 (39%), Gaps = 109/382 (28%)

Query: 30 PYRRPRFLRGSSSSPGAADASRRPDSRPV-RSPARGRTL PWNAGYAEIINAEKSEFNEDQ 88
P +R R R +S +P RPD P+ GRT EF +
Sbjct: 55 PGKRQRLARTASGAP-----RPDEDSASERPSCGRT-----EEF--PR 90

Query: 89 AACGKLCIRRCEFGAEEEWLTLCPEEFITG----HYWALFDGHGGPAAAILAANTLHSL 144
+C RR E E+ +++ P+ FL H++ +FDGHG A + +H +
Sbjct: 91 YGVTAVCGRRREM---EDAVSIRPD-FLPASGKFHFYGVFDGHGCSHVATTCQDRMHEIV 146

Query: 145 RRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGALESFAFQECDEVIG 204
+ G VA P + + D + R++D E
Sbjct: 147 AEEHNKGASGEVA--PWRDVMKESFARMGDEVGNRASTRSDDEPACPCE----- 193

Query: 205 RELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEEFTPETERQRIQQ 264
++ + G TA+VAV ++ +ANAGDSRA++ R LS + P+
Sbjct: 194 QQTSPRRDHAGSTAVVAVVSPTQVVVANAGDSRAVISRAGVPVALSVDHKPDR----- 246

Query: 265 LAFVYPELLAGEFTRLEFPRLKGGDLGQKVLFRDHMSGWSYKRVEKSDLKYPLIHGQG 324
P+ E R+E G +V++ D
Sbjct: 247 -----PD-----ELERIEAA-----GGRVIYWD----- 264

Query: 325 RQARLLGTLAVSRGLGDHQLRVLDNTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATD 384
AR+LG LA+SR +GD L KP++ S P+VTV + +D+ +++A+D
Sbjct: 265 -GARVLGVLAMSRAIGDGYL-----KPYVTSEPEVTVTE----RTDDDECLILASD 310

Query: 385 GLWDVLSNEQVAWLVRSLPGN 406
GLWDV++NE +VR+ N
Sbjct: 311 GLWDVVTNEMACEVVRACFHNN 332

>gi|30693757|ref|NP_175057.2| protein phosphatase 2C (PP2C), putative
[Arabidopsis thaliana]
gi|17381034|gb|AAL36329.1| putative protein phosphatase type 2C
[Arabidopsis thaliana]
gi|21436259|gb|AAM51268.1| putative protein phosphatase type 2C
[Arabidopsis thaliana]
Length = 371

Score = 66.6 bits (161), Expect = 8e-10
Identities = 59/212 (27%), Positives = 86/212 (40%), Gaps = 68/212 (32%)

Query: 191 ALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLS 250
A+ F++ DE E + G TA A + KL +AN GDSR + R PLS
Sbjct: 191 AIVEVFKQTDEEYLIEEAGQPKNAGSTAATAFLIGDKLIVANVGDSRVVASRNGSAVPLS 250

Query: 251 FEFTPE--TERQRIQQLAFVYPELLAGEFTRLEFPRLKGGDLGQKVLFRDHMSGWSYK 308
+ P+ ERQRI +D G +++ W
Sbjct: 251 DDHKPDRSDERQRI-----EDAGGFIIW----AGTW--- 277

Query: 309 RVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKPFLLSVPQVTVLDV 368
R+ G LAVSR GD QL KP++++ P++ D+
Sbjct: 278 -----RVGGILAVSRAFGDKQL-----KPYVIAEPEIQEEDI 309

Query: 369 DQLELQEDDVVVMATDGLWDVLSNEQVAWLVR 400
LE +V+A+DGLW+VLSN+ +VR
Sbjct: 310 STLEF-----IVVASDGLWNVLSNKDAVAIVR 336

>gi|34902050|ref|NP_912371.1| putative Serine/threonine phosphatases [Oryza sativa (japonica cultivar-group)]
gi|29893648|gb|AAP06902.1| putative Serine/threonine phosphatases [Oryza sativa (japonica cultivar-group)]
gi|29893658|gb|AAP06912.1| unknown protein [Oryza sativa (japonica cultivar-group)]
Length = 404

Score = 66.6 bits (161), Expect = 1e-09
Identities = 89/338 (26%), Positives = 130/338 (38%), Gaps = 99/338 (29%)

Query: 78 NAEKSEFNEDQAACGKLCIRRCEFGAEEEWLTLCPPEEFLTGH-YWALFDGHGGPAAAILA 136
+ E E + +C RR + E+ ++ CP FL GH ++ +FDGHG A
Sbjct: 67 DEEDREVERARYGFTSVCGRRRDM---EDSVSACPG-FLPGHHFFGVFDGHGCSHVAT-- 120

Query: 137 ANTLHSLRRLQLEAVVEGLVATQPPMHLNG-----RCICPSDPQFVEEKGIRAEDL 187
SC +R E VV+ A L+ R D + V
Sbjct: 121 -----SCGQRMHEIVVDEAGAAAGSAGLDEEARWRGVMERSFARMDAEAVASSRGSVAPA 175

Query: 188 VIGALESFAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIR 247
E +CD V G TA+VAV + +AN GDSRA+L R
Sbjct: 176 PTCRCQMQLPKCDHV-----GSTAVVAVLGRHVVVANCGDSRAVLCRGGAAI 223

Query: 248 PLSFEFTPE--TERQRIQQLAFVYPELLAGEFTRLEFPRLKGDGLGQKVLFRDHHMSGW 305
PLS + P+ E +RI G +V+F D
Sbjct: 224 PLSCDHKPDRLPELERIHAA-----GGRVIFWD----- 251

Query: 306 SYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNQLKPFLLSVPQVTV 365
AR+ G LA+SR +GD L KP+++ P+V V
Sbjct: 252 -----GARVFGMLAMSRAIGDSYL-----KPYVICDPEVRV 282

Query: 366 LDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSL 403
++ ED+ +++A+DGLWDV+SNE +VR+ L
Sbjct: 283 MERKD---GEDEFLILASDGLWDVVSNEVACNVVRACL 317

>gi|26331022|dbj|BAC29241.1| unnamed protein product [Mus musculus]
gi|26337573|dbj|BAC32472.1| unnamed protein product [Mus musculus]
Length = 360

Score = 66.2 bits (160), Expect = 1e-09
Identities = 75/315 (23%), Positives = 122/315 (38%), Gaps = 96/315 (30%)

Query: 121 WALFDGHGGPAAAILAANTLHSLRRLQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEK 180

```

      + +FDGHGG  AA      + L    L++ L+          D +  +E
Sbjct: 124 FGIFDGHGGETA AEYVKSRLPEALKQHLQ-----DYEKDKEN 160

Query: 181 GIRAEDLVIGALES AFQECDE VIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAIL 240
      +      +  LE      D +  +L S    G T L+A+      L +AN GDSR +L
Sbjct: 161 SVLTYQTI---LEQQILSIDREMLEKLT VSYDEAGTTCLIALLSDKDLTVANVGDSRGVL 217

Query: 241 VRRD-EIRPLSFEEFTPET--ERQRIQQ LAFVYPELLAGEFTRLEFP RRLKGDDL GQKVL F 297
      +D      PLS +  P      ER+RI++          AG F
Sbjct: 218 CDKDGNAIPLSHDHKPYQLKERKRIKR-----AGGFISFN-----252

Query: 298 RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TN IQLKPFL 357
      W                                R+ G LA+SR LGD+ L+ L+      +
Sbjct: 253 -----GSW-----RVQGILAMSRSLGDYPLKNLNV-----V 278

Query: 358 LSV PQVT VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR SF L PGNQEDPHRF SKLA 417
      + P +  D+D+L+      + +++A+DGLWD SNE+      ++ L      ++PH F  +
Sbjct: 279 IPDPDILT FDLDKLQ---PEFMILASDGLWDAFSNEEAVRFIKERL----DEPH-FGAKS 330

Query: 418 QMLIHSTQGKEDSLT 432
      +L      +G  D++T
Sbjct: 331 IVLQSFYRGCPDNIT 345

```

>gi|34857062|ref|XP_227247.2| similar to protein phosphatase 2C epsilon
[Rattus norvegicus]
Length = 360

Score = 65.9 bits (159), Expect = 1e-09

Identities = 75/315 (23%), Positives = 122/315 (38%), Gaps = 96/315 (30%)

```

Query: 121 WALFDGHGGPAAAAILAANTLHSC LRRQLEAVVEGLVATQPPMHLN GRCICPSDPQFVEEK 180
      + +FDGHGG  AA      + L    L++ L+          D +  +E
Sbjct: 124 FGIFDGHGGETA AEYVKSRLPEALKQHLQ-----DYEKDKEN 160

Query: 181 GIRAEDLVIGALES AFQECDE VIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAIL 240
      +      +  LE      D +  +L S    G T L+A+      L +AN GDSR +L
Sbjct: 161 SVLTYQTI---LEQQILSIDREMLEKLT VSYDEAGTTCLIALLSDKDLTVANVGDSRGVL 217

Query: 241 VRRD-EIRPLSFEEFTPET--ERQRIQQ LAFVYPELLAGEFTRLEFP RRLKGDDL GQKVL F 297
      +D      PLS +  P      ER+RI++          AG F
Sbjct: 218 CDKDGNAIPLSHDHKPYQLKERKRIKR-----AGGFISFN-----252

Query: 298 RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TN IQLKPFL 357
      W                                R+ G LA+SR LGD+ L+ L+      +
Sbjct: 253 -----GSW-----RVQGILAMSRSLGDYPLKNLNV-----V 278

Query: 358 LSV PQVT VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR SF L PGNQEDPHRF SKLA 417
      + P +  D+D+L+      + +++A+DGLWD SNE+      ++ L      ++PH F  +
Sbjct: 279 IPDPDILT FDLDKLQ---PEFMILASDGLWDAFSNEEAVRFIKERL----DEPH-FGAKS 330

Query: 418 QMLIHSTQGKEDSLT 432
      +L      +G  D++T
Sbjct: 331 IVLQSFYRGCPDNIT 345

```

>gi|31197933|ref|XP_307914.1| ENSANGP00000021879 [Anopheles gambiae]
 gi|21291512|gb|EAA03657.1| ENSANGP00000021879 [Anopheles gambiae str.
 PEST]

Length = 467

Score = 65.5 bits (158), Expect = 2e-09

Identities = 76/284 (26%), Positives = 111/284 (39%), Gaps = 97/284 (34%)

Query: 120 YWALFDGHGGPAAAILAANTLHSCLRRLQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEE 179
 ++A++DGHGG A A LH + R+ P++ +

Sbjct: 68 FFAVYDGHGGAKVAEYAGKHLHKYVTRR-----PEYGND 101

Query: 180 KGIRAEDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAI 239
 V AL+ F + DE + QM G TA+V + +LY ANAGDSRAI

Sbjct: 102 -----VKHALQQGFLDLDEAMLNNEALREQMSGSTAVVVLKDNRLYCANAGDSRAI 153

Query: 240 LVRRDEIRPLSFEFTP--ETERQRIQQLAFVYPELLAGEFTRLEFPRLKGDGQKVLV 297
 + LSF+ P E ER+RI AG +

Sbjct: 154 ACVDGRDLVLSFDHKPTNEKERERISS-----AGGYVE----- 186

Query: 298 RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNLQKPF 357
 Y RV G LA+SR LGD L+ + I+ K +

Sbjct: 187 -----YNRVN-----GYLALSRALGDFGLK-RNKQIEAKEQM 217

Query: 358 LSVPPQVTVLDDVDQLELQED-DVVVMATDGLWDVLSNEQVAWLVR 400

++ DV++ E+ E D +V+A DG+WDVLS++ V V+

Sbjct: 218 VT-----AYPDVEEREVSEGWDFLVIACDGIWDVLSQAVLEFVQ 257

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
 Posted date: Dec 22, 2003 2:26 AM
 Number of letters in database: 518,058,112
 Number of sequences in database: 1,581,064

Lambda	K	H
0.319	0.137	0.418

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 49,488,909

Number of Sequences: 1581064

Number of extensions: 2209022

Number of successful extensions: 7773

Number of sequences better than 10.0: 60

Number of HSP's better than 10.0 without gapping: 32

Number of HSP's successfully gapped in prelim test: 28

Number of HSP's that attempted gapping in prelim test: 7639
Number of HSP's gapped (non-prelim): 127
length of query: 459
length of database: 518,058,112
effective HSP length: 128
effective length of query: 331
effective length of database: 315,681,920
effective search space: 104490715520
effective search space used: 104490715520
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.8 bits)
S2: 75 (33.5 bits)

>gi|39573724|ref|NP_945149.1| protein phosphatase 2C eta isoform 2; protein phosphatase 2C eta

[Mus musculus]

gi|37704769|gb|AAR01612.1| protein phosphatase 2C eta [Mus musculus]

Length = 406

Score = 704 bits (1816), Expect = 0.0

Identities = 345/387 (89%), Positives = 366/387 (94%), Gaps = 3/387 (0%)

Query: 76 IINAEKSEFNEDQAACGKLCIRRCEFGAEE--EWLTLCPEEFLTGHYWALFDGHGGPAAA 133
+INAEKSEFNEDQAACGKLCIRRCEFG EE EWLT+CPEEFLTGHYWALFDGHGGPAAA

Sbjct: 20 VINA EKSEFNEDQAACGKLCIRRCEFGIEEDQEWLTVCP EEF LTGHYWALFDGHGGPAAA 79

Query: 134 ILAANTLHSLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGALE 193
ILAANTLHSLRRQLEAVVEG++A QPPMHL+GRC+CPSDPQFVEEKGI+AEDLVIGALE

Sbjct: 80 ILAANTLHSLRRQLEAVVEGMMAPQPPMHLSGRCVCPSDPQFVEEKGIQAEDLVIGALE 139

Query: 194 SAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEF 253
+AFQECD+VIGRELEASGQ+GGCTALVAV LQGKLY+ANAGDSRAILVRR EIR LS EF

Sbjct: 140 NAFQECDDVIGRELEASGQVGGCTALVAVFLQGKLYVANAGDSRAILVRRHEIRQLSSEF 199

Query: 254 TPETERQRIQQALAFVYPELLAGEFTRLEFPRLKGDDLQKQVLF RDHHMSGWSYKRVEKS 313
TPETERQRIQQALAF YPELLAGEFTRLEFPRLKGDDLQKQVLF RDHHM GWSYKRVEKS

Sbjct: 200 TPETERQRIQQALAFVYPELLAGEFTRLEFPRLKGDDLQKQVLF RDHHMRGWSYKRVEKS 259

Query: 314 DLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TN IQLKPFLLSVPQVTVLDVDQLEL 373
DLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD T+IQLKPFLLS+PQVTVLDV QL +

Sbjct: 260 DLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD TDIQLKPFLLSIPQVTVLDVHQLAV 319

Query: 374 QEDDVVVMATDGLWDVLSNEQVAWLVR SFLPGNQ-EDPHRFSKLAQMLIHSTQGKEDSLT 432
QE+DVVVMATDGLWDVLSNEQVA LVR SFL GNQ +DPHRFS+LA+MLIH+TQ GK++ T

Sbjct: 320 QEEDVVVMATDGLWDVLSNEQVALLVR SFLTGNQKDDPHRFSELAQMLIHNTQ GKDN GAT 379

Query: 433 EEGQVS YDDVSVFVIPLHSQGQESSDH 459

EEGQVS YDDVSVFVIPLHSQ QE S H

Sbjct: 380 GEGQVS YDDVSVFVIPLHSQAQEGSGH 406

Short sequence-paper

Molecular cloning of PP2C η , a novel member of the protein phosphatase 2C family[☆]Ken-ichiro Komaki^{a,b}, Koji Katsura^c, Motoko Ohnishi^d, Ming Guang Li^a, Masato Sasaki^a,
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Abstract

We have cloned a novel member of the mouse protein phosphatase 2C family, PP2C η . Sequence analysis suggests that PP2C η , PP2C ζ and NERPP-2C constitute a unique subgroup of the PP2C family. PP2C η had extremely low activity against α -casein compared with PP2C α and was localized mainly in cell nuclei, suggesting that PP2C η dephosphorylates a unique nuclear protein(s) in the cells.

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Keywords: Protein phosphatase 2C; Cloning; Motif; Expression; Enzyme activity; Subcellular localization

Protein phosphorylation plays key roles in the regulation of cellular functions, and protein phosphatases in combination with protein kinases control the phosphorylation levels of cellular proteins. Protein Ser/Thr phosphatases (PP) of eukaryotes are classified into two families (PPP and PPM), which are defined by distinct amino acid sequences and three-dimensional structures [1]. Protein phosphatase 2C (PP2C) and pyruvate dehydrogenase phosphatase (PDHPase) belong to the PPM family, while PP1, PP2A and PP2B belong to the PPP family. To date, at least 10 different PP2C genes have been identified in mammalian cells [2–16]. In addition, two splice variants of PP2C α [17,18] and six splice variants of PP2C β have been identified [2,19–23]. Structurally, all 10 distinct PP2C gene products share six conserved motifs that are also conserved in most of the PP2C gene products from a variety of other species. All

of these PP2Cs have Mg²⁺- and/or Mn²⁺-dependent protein phosphatase activities against artificial substrates in vitro. Recent progress in the genome and EST sequencing projects has revealed that *Saccharomyces cerevisiae*, *Drosophila melanogaster*, *Caenorhabditis elegans* and *Mesembryanthemum crystallinum* (ice plant) have 8, 12, 9 and 10 different PP2C genes, respectively [24,25]. In addition, it has been reported that 69 different PP2C genes exist in *Arabidopsis thaliana* [26]. Structural studies of PP2C from these species have revealed that some of these phosphatases contain motifs such as the kinase interaction domain of KAPP (*A. thaliana*) and the transmembrane domain of KAPP and MPC8 (ice plant), which have not been observed in mammalian PP2C family members [25,27]. These observations raise the possibility that mammalian cells, whose genomic complexity is larger than that of other species, may contain a number of unidentified PP2C genes. Indeed, we now describe the molecular cloning of PP2C η , a novel member of the mammalian PP2C family.

The restriction enzymes and other modifying enzymes used for DNA manipulation were obtained from Takara (Kyoto, Japan). Synthesized oligonucleotides were consigned to HSS (Hokkaido, Japan). Antihemagglutinin (HA) antibody (12CA5) was obtained from Roche Molecular Biochemicals (Mannheim, Germany). Antimouse IgG

Abbreviations: PP2C, protein phosphatase 2C; NLS, nuclear localization signal; OA, okadaic acid

[☆] Nucleotide sequence data for PP2C η cDNA is available in GenBank database under the accession number AY332616.

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and HRP-linked antibody were purchased from Cell Signaling Technology (Beverly, USA). Alexa Fluor 488-conjugated goat antimouse IgG was purchased from Molecular Probes (Eugene, USA). Cy3-conjugated goat antirabbit IgG was purchased from Jackson ImmunoResearch (West Grove, USA). Hoechst 33258 and monoclonal anti- α -tubu-

lin clone DM 1A were obtained from Sigma (St. Louis, USA). Amylose resin was from New England Biolabs (Ontario, Canada). Hybond-P, Hybond-N+ and ECL kits were obtained from Amersham Biosciences (Uppsala, Sweden). [α - 32 P]dCTP and [γ - 32 P]ATP were obtained from Perkin Elmer Life Sciences (Tokyo, Japan). Dulbecco's

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1  CCTGCGTTCCTCCAGACCCTCTGCCTGATCCCGTCTGGTTCTGTGCTGACCTGGAAAACCG
63  ACGGGGTGTGCACATCCCCGCTAACCTTCTTCTGTCTTCAACCTTGACAGCATTTCTCTTT
125  TTTCTCACTTTGGCAITTTCTTTTGAGAAGGTGGAGGTCCCCGGGAGGGCTCGACCCGGC
187  TGGACCCTCCTTCTTCTGGCCTCTGCAGATGTATGTCCACCTCGCACCTCACTTAGGGT
      M Y V P P R T S L R V 11
249  TGGCCTATGCTCTGTGGGATAAGGGTTATCAATGCAGAAAAATCTGAATTCGAAGACCA
      W P M L C G I R V I N A E K S E F N E D Q 32
311  GGCTGCTTGGCGGAAGCTATGCATCCGGCGATGTGAGTTTGGGATCGAAGAAGATCAAGAGT
      A A C G K L C I R R C E F G I E E D Q E W 53
373  GGCTGACGGTGTGCCAGAGGAGTTCTGACGGGTCACTACTGGGCACTGTTTGATGGGCAT
      L T V C P E E F L T G H Y W A L F D G H 73
435  GGTGGCCCTGCTGCAGCTATCTTGGCTGCCAACACCCTGCACTCTTGCCCTCGCCGGCAGCT
      G G P A A A I L A A N T L H S C L R R Q L 94
497  GGAGGCTGTGGTTGAAGGCATGATGGCCCTCAGCCCCCATGCACCTCAGTGGCCGCTGTG
      E A V V E G M M A P Q P P M H L S G R C V 115
559  TCTGCCCCAGTGACCCCCAGTTCGTGGAGGAAAAGGGGATCCAGGCAGAAGACTTGGTGATC
      C P S D P Q F V E E K G I Q A E D L V I 135
621  GGGGCTCTGGAGAACGCCTTCCAGGAATGTGATGATGTGATTGGGAGAGAGCTGGAGGCCTC
      G A L E N A F Q E C D D V I G R E L E A S 156
683  AGGACAGGTGGGTGGCTGTACAGCCCTGGTGGCGGTGTTCTGCAAGGGAAGCTGTATGTGG
      G Q V G G C T A L V A V F L Q G K L Y V A 177
745  CCAATGCTGGGGACAGCAGGGCCATCTTGGTGGGAGACATGAGATACGGCAGCTGAGTTCT
      N A G D S R A I L V R R H E I R Q L S S 197
807  GAGTTACCCAGAAACAGAGCGGCAGCGGATCCAGCAGCTGGCCTTTACCTACCTGAGCT
      E F T P E T E R Q R I Q Q L A F T Y P E L 218
869  TCTGGCTGGAGAGTTCACCCGACTGGAGTTCACCGCGGGCTAAAGGGGGATGACTTAGGGC
      L A G E F T R L E F P R R L K G D D L G Q 239
931  AGAAGGTTTTGTTTCAGGGATCATCATGAGAGGCTGGAGCTACAAACGGGTGGAAAAGTCT
      K V L F R D H H M R G W S Y K R V E K S 259
993  GATCTCAAGTATCCACTGATTCATGGACAGGGTAGGCAGGCGGTTACTGGGAACACTGGC
      D L K Y P L I H G Q G R Q A R L L G T L A 280
1055  TGTCTCCAGAGGGCTGGGCGACCATCAGCTTAGAGTCTGGACACCGACATCCAGCTGAAGC
      V S R G L G D H Q L R V L D T D I Q L K P 301
1117  CCTTCTACTCTCCATCCACAGGTGACTGTGCTGGATGTCCACCAGCTGGCAGTGCAGGAG
      F L L S I V P Q V T V L D V H O L A V Q E 321
1179  GAGGATGTGGTTGTATGGCAACTGATGGGCTCTGGGATGTCTGTCCAATGAGCAGGTGGC
      E D V V V M A T D G L W D V L S N E Q V A 342
1241  ACTGCTTGTGCGGAGCTTCTCACCGGGAACCAAAAGGATGACCCACACAGGTTCTCAGAGT
      L L V R S F L T G N Q K D D P H R F S E L 363
1303  TGGCCAAAATGCTGATACACAACACTCAAGGAAAGGACAATGGTGCCACCGGAGAGGGGCAG
      A K M L I H N T Q G K D N G A T G E G Q 383
1365  GTATCCTACGACGATGTCTCCGTGTTGTGATTCCTTTGCACAGCCAGGCCCAAGAAGGCAG
      V S Y D D V S V F V I P L H S Q A Q E G S 404
1427  TGGCCACTGAGGGCTCACATACTGCGTTCTAGAACCTCCTCAGGACCAGTGCAGACTCAGCA
      G H * 406
1489  TATGTCCACTGTGGCCAAGGCAGGCCCTGCCTGGCCTGTTCAAAGCCACAGCCCAATGCTT
1551  ACCAGGTCCCACCTTCTGCAATGGTAACATTCCCTGGCAGAGTACTTGATAGCACATGGC
1613  ATCTGTGTTAGCGCTCTGCAGGATAAATGGTTAAGGGCACTATGAAGTCTTGGGGAGCAGG
1675  AACTCTGGGTCCAACCTCGTGAATCTCAAGTTATTATTCATTTAACCATCCATCCACACAAG
1737  GCACCTTCTTGAAACCTCTGGGCAGTCTCACATTGCTTAATTTAATTAAGATTAAAGCGGT
1799  CTTAATTTTTTCTTC

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Fig. 1. Nucleotide and predicted amino acid sequence of PP2C η . Nucleotides are numbered on the left and amino acids are numbered on the right. The open reading frame starting at position 216 and ending at position 1434, marked by an asterisk, encodes 406 amino acids. Underlines indicate the predicted six conserved motifs of PP2C η . The basic amino acids composing the putative nuclear localization signal are double underlined.

modified Eagle's medium (DMEM) and Lipofectamine were purchased from Gibco BRL (Rockville, USA). All other reagents used were obtained from Wako Pure Chemical (Osaka, Japan).

We searched the EST database for DNA clones encoding the amino acid sequences of the unique motifs conserved in mouse PP2C family members. Three different clones, each potentially encoding a novel member of the PP2C family, were identified. These three cDNAs were designated clone-1 [9], -2 [10] and -3. A putative full-length cDNA of clone-3 was obtained by 5' and 3' RACE methods using the total RNA fraction isolated from 13.5-day mouse embryo as the template. The first strand cDNA was synthesized with SuperScript II RT (Gibco BRL) using oligo(dT) primer, 5-GGCCACGCGTCGACTAGTACTTTTTTTTTTTT-

TTTTT-3'. Next, an adapter primer, 5'-GGCCACGCGTC-GACTAGTAC-3', and gene-specific primer (GSP): GSP1, 5'-TTACCTACCCTGAGCTTCTG-3', or nested GSP1, 5'-GATGACTTAGGGCAGAAGG-3', were used in 3' RACE. 5' RACE was carried out using the 5' RACE System for Rapid Amplification of cDNA Ends, Version 2.0 (Gibco BRL). The 5' RACE was conducted according to the manufacturer's instructions. The first strand cDNA was synthesized with SuperScript II RT (Gibco BRL) using GSP2, 5'-TAGGAAGGGCTTCAGCTGG-3', and then the universal amplification primer (UAP) contained in this kit and GSP: GSP3, 5'-ACAGCCAGTGTCCAGTA A-3', nested GSP3, 5'-CTGTCCATGAATCAGTG-3', GSP4, 5'-CAAGATGGCCCTG CTGTC-3', nested GSP4, 5'-AGCTCTCTCCCAATCACATC-3', GSP5, 5'-CAC-

	<u>Motif I</u>	<u>Motif II</u>	<u>Motif III</u>	
mPP2C α	RVEMED 38	FFAVYDGHAG 64	GSTAVGVLSIPQHTYFINGDSRGLL 151	
mPP2C β	RVEMED 38	FFAVYDGHAG 64	GSTAVGVMVSPHMYFINGDSRAVL 156	
mCaMKPas e	RRKMED 167	YFAVFDGHGG 198	GTTGVCALIAAGALHVAWLGDSSQVIL 276	
hPOPX1	RRKMED 248	YFAVFDGHGG 279	GTTGVVTFIRGNMLHVAWVGDSQVML 356	
mFIN13	RVS MED 41	MFSVYDGHGG 64	GTTAVVALIRGKQLIVANAGDSRCVV 350	
hILKAP	REEMQD 123	YFAVFDGHGG 156	GSTATCVLAVDNILYIANLGDSRAIL 241	
mPP2C ϵ	RDH MED 50	IFGIFDGHGG 75	GTTCLIALLSDKDLTVANVGDSRGVL 160	
mWip1	RKY MED 23	FFAVCDGHGG 102	GTTASVVIIRGMKMYVAHVGDGSGVVL 190	
mPP2C ζ	KSRH NED 120	YWGLFDGHAG 163	GCCALVLYLLGKMYVANAGDSRAII 285	
hNERPP-2C	KSTH NED 78	YWSLFDGHAG 139	GCTALIVICLLGKLYVANAGDSRAII 277	
mPP2C η	KSEF NED 31	YWALFDGHGG 75	GCTALVAVFLQGKLYVANAGDSRAIL 186	
hP DHPas e	ANAPIED 161	LLGVFDGHAG 184	GATACVAHVVDGVDLHVANTGDSRAML 332	
	<u>Motif IV</u>	<u>Motif V</u>	<u>Motif VI</u>	
mPP2C α	RVN ————— GSLAVSRALGDF 200	PEVHDIERSEEDDQFII— LAC-DGIWD 243	DNMSVILICF 291	
mPP2C β	RVN ————— GSLAVSRALGDY 205	PEVYEIVRAEEDF-FVV— LAC-DGIWD 247	DNMSVVLVCF 295	
mCaMKPas e	RVN ————— GTLAVSRAIGDV 328	ADAASRELTGSED-YLL— LAC-DGFFD 361	DNITVMVVFL 410	
hPOPX1	RVN ————— GSLSVSRAIGDA 408	ADSASTVLDGTED-YLI— LAC-DGFYD 441	DNITVIVVFL 490	
mFIN13	RVN ————— GGLNLSRAIGDH 400	PDIKVLTLT-DDHEFMV— IAC-DGIWN 442	DNMTCHICF 502	
hILKAP	RVL ————— GVLEVSRSIGDG 296	PDIRRCQLTPNDR-FIL— LAC-DGLFK 330	DNVTVMVVRI 390	
mPP2C ϵ	RVQ ————— GILAMSRSLGDY 213	PDILTFDLDKLQPEFMI— LAS-DGLWD 249	DNITVMVVKF 294	
mWip1	GVNRVVWKRPRLTHSGPVRSTVIDQIPFLAVARALGDL 271	PEPDTSVHTLDPKHKYI-IL GSDGLWN 311	DNTSAIVICI 368	
mPP2C ζ	RVM ————— ATIGVTRGLGDH 387	PEVRVYDLTQYEHCPDDVLVLGTDGLWD 433	DDISVFVIPL 499	
hNERPP-2C	RVM ————— ATIGVTRGLGDH 379	PEVRIYDLISKYDHGSDDLILATDGLWD 425	DDISVYVIPL 491	
mPP2C η	RLL ————— GTLAVSRGLGDH 288	PQVTVLVDVHQLAVQEEDVVMATDGLWD 334	DDVSFVIPL 396	
hP DHPas e	RLL ————— GLLMPFRAFGDV 392	PEVTYHRLR-PQDKFL— VLATDGLWE 458	DDITIIVVQF 561	

Fig. 2. Comparison of the amino acid sequences of the six conserved motifs of PP2C η with those of other PPM family members. The alignment of amino acid sequences within each of the six conserved motifs (I–VI) of the 12 PPM members is shown. PP2C α [31], PP2C β [19], CaMKPas e [GenBank™, BC042570], FIN13 [6], PP2C ϵ [9], Wip1 [GenBank™, AF200464], PP2C ζ [10], and PP2C η are murine proteins while POPX1 [15], ILKAP [8], NERPP-2C [GenBank™, XM_051093] and PHDPas e [GenBank™, AF155661] are human proteins. Numbers on the right identify the amino acid position for each protein. The amino acids, which participate in the binding of metal ions, are marked in boldface [1].

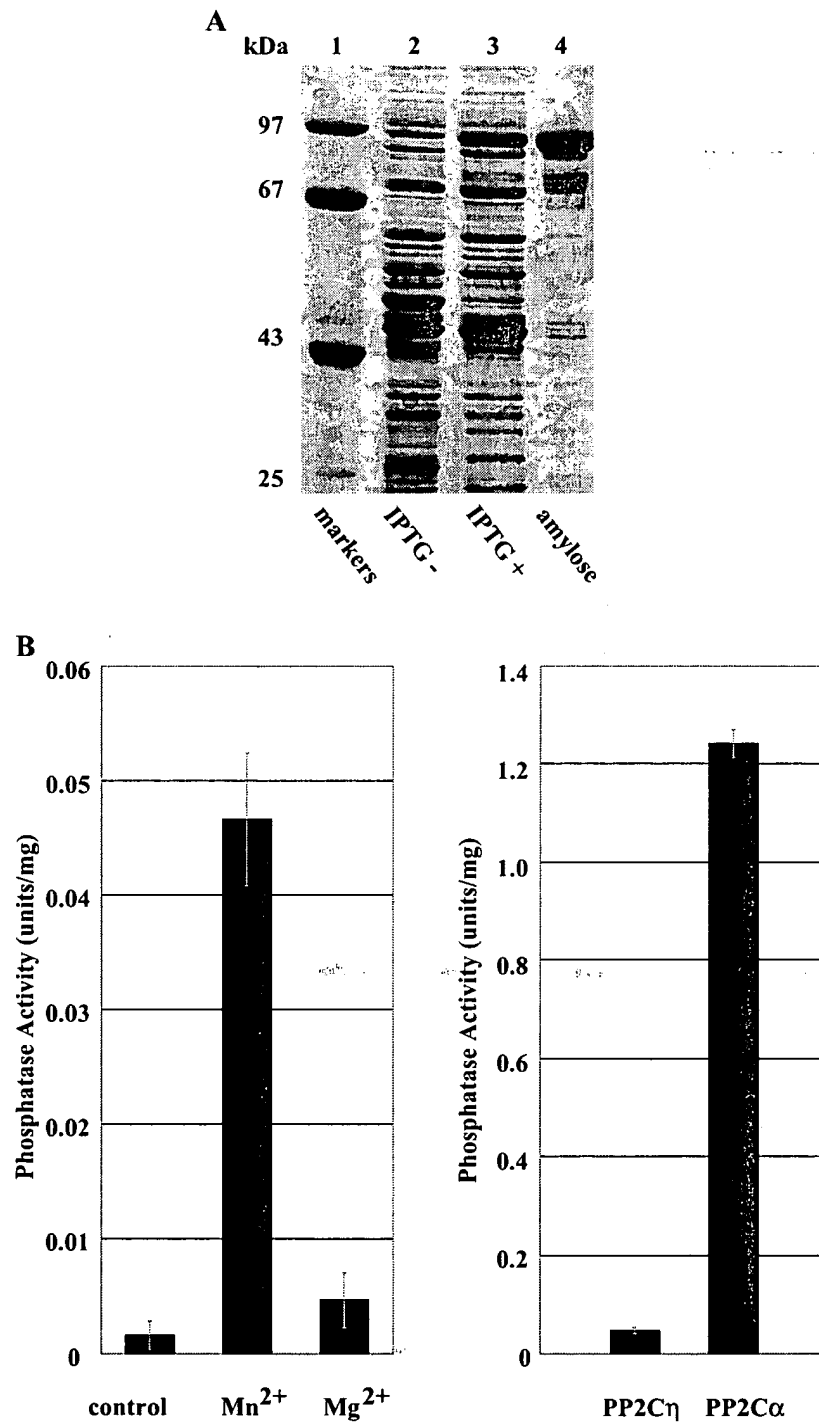


Fig. 3. Protein phosphatase activity of recombinant PP2C η expressed in *E. coli* cells. (A) *E. coli* (DH5 α) cells were transformed with the MBP-PP2C η expression plasmid and expression was induced by IPTG. The expressed MBP-PP2C η was purified by amylose resin from the cell lysates. *E. coli* cell lysates without (lane 2) or with (lane 3) IPTG treatment and the purified MBP-PP2C η (lane 4) were subjected to 10% SDS-PAGE and stained with Coomassie Brilliant Blue. Molecular size markers are shown in lane 1. (B) Phosphatase activity was assayed using ³²P-labeled casein as the substrate in the presence of 1 μ M OA with or without 10 mM MgCl₂ or 10 mM MnCl₂ (left panel). The specific activity of MBP-PP2C η was compared with that of MBP-PP2C α in the presence of 10 μ M OA and 10 mM MnCl₂ (right panel).

CATGCCCATCAAACAG-3', or nested GSP5, 5'-CATAGGCCAAACCCTAA GTG-3', were used in the 5' RACE.

For bacterial expression of proteins, the PP2C η and PP2C α cDNAs were subcloned into pMAL-c2X (New England Biolabs) to generate maltose binding protein (MBP)-PP2C η and MBP-PP2C α fusion proteins. For expression of PP2C η in mammalian cells, the PP2C η cDNA was subcloned into the pCX expression vector [28]. An HA tag was added to the construct using synthesized oligonucleotides and the resulting plasmid was named pCX-HA-PP2C η . MBP-PP2C η and MBP-PP2C α were expressed in the *E. coli* DH5 α strain. The expressed proteins were purified from cell extracts using amylose resin.

α -Casein was phosphorylated using protein kinase A and [γ - 32 P]ATP as described previously [29,30]. The reaction mixture was gel filtered with Sephadex G-25 and the isolated 32 P-labeled casein was stored at -20°C until use. Casein phosphatase activity was assayed by measuring the release of 32 P inorganic phosphate from 32 P-labeled casein, essentially as described previously [29].

Total RNA was extracted from mouse tissues with RNA-Bee (Tel-Test, Inc., Texas, USA). The denatured RNA (20 μg) was electrophoresed in a 1.0% (w/v) agarose gel, transferred onto a Hybond-N+ membrane, and Northern hybridization was carried out as described previously [19]. A 32 P-labeled probe representing the entire coding sequence of the PP2C η cDNA was used for the hybridization.

293IL-1RI cells were grown in DMEM supplemented with 10% (v/v) fetal bovine serum. For stable transfections, 293IL-1RI cells were co-transfected with pBABE, encoding the puromycin resistant gene, and pCX-HA-PP2C η or pCX vector using Lipofectamine. Puromycin-resistant colonies were isolated. For immunoblot analysis, the cell extracts were subjected to 10% (w/v) SDS-PAGE and then transferred onto polyvinylidene difluoride membrane. The membrane was incubated with the primary antibody for 1 h at 25°C , then incubated with the secondary antibody for 30 min at 25°C . The immunore-

activity was detected with an ECL kit. For indirect immunofluorescence analysis, the cells were cultured on poly-L-lysine coated cover glass and then fixed with 4% (w/v) paraformaldehyde for 15 min. The fixed cells were permeabilized with 0.1% (v/v) Triton X-100, blocked with PBS containing 2% (v/v) normal goat serum and incubated with the primary antibody for 1 h at 25°C . The cells were then incubated with the secondary antibody for 1 h at 25°C and with Hoechst 33258. Confocal microscopic analysis was performed with a Zeiss LSM410 microscope (Carl Zeiss, Jena, Germany).

The isolated cDNA clone (clone-3) contained a single oligonucleotide of 1813 bp (Fig. 1). We concluded that the Met codon at position 216 was likely to be the translation initiation codon, because the 5' upstream sequence contained an in-frame stop codon. The first stop codon downstream of the putative translation initiation codon was at position 1436. The open reading frame of the cDNA clone encoded a polypeptide of 406 amino acid residues. The primary structure of the encoded protein contained the six motifs (I–VI), which are conserved in all known mammalian PP2C family members (Fig. 2). These results suggested that the encoded protein was a novel member of the PP2C family and it was designated PP2C η . A unique feature of the primary structure of PP2C η was the presence of a putative nuclear localization signal (NLS) rich in basic amino acids in the region between motifs III and IV (Fig. 1).

The 10 mammalian PP2C family members previously reported were classified into two subgroups depending on the difference in the amino acid sequence of motif I (Fig. 2) [2]. Group 1 PP2Cs (PP2C α , PP2C β , FIN13/PP2C γ , PP2C δ , PP2C ϵ , Wip1, CaMKPase/POPX2 and CaMKPase-N/POPX1) contained the sequence RXXME/QD in motif I, whereas group 2 PP2Cs (PP2C ζ and NERPP-2C) contained the sequence KXXXNED in motif I. No notable difference was observed in the amino acid sequences of motifs II–VI between groups 1 and 2. PDHPase, another member of the PPM family, also contained the six conserved motifs (Fig. 2). However, the basic amino acid (R or

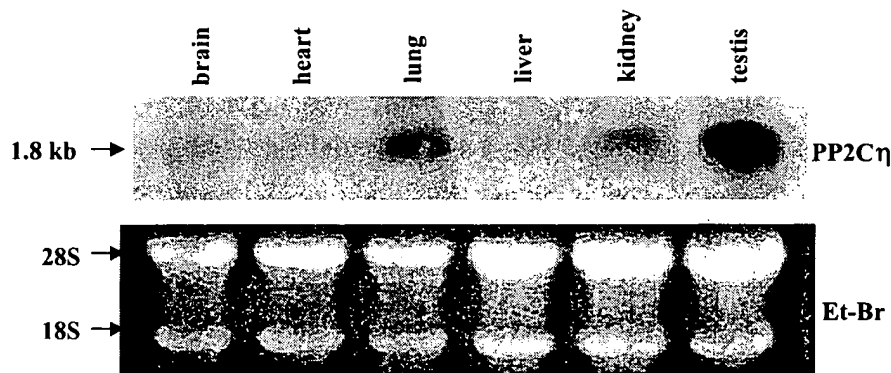


Fig. 4. Northern blot analysis. Total RNA fractions (20 μg) obtained from the indicated mouse tissues were separated in a 1% (w/v) agarose gel. After staining with ethidium bromide (lower panel), the RNAs were transferred to a nylon membrane and hybridized with a random primed 32 P-labeled full length PP2C η cDNA probe (upper panel). The positions of PP2C η mRNA (upper panel) and 28 S and 18 S rRNA (lower panel) are shown.

K) contained in motif I of the groups 1 and 2 of the PP2C family was not observed in the corresponding positions of motif I of PDHPae. The sequence KXXXNED was identified in motif I of PP2C η (Lys²⁵–Asp³¹). In addition, PP2C η shared 43% and 38% amino acid similarity with PP2C ζ and NERPP-2C, respectively, while it shared only 16–21% similarity with the group 1 members. NERPP-2C described in Fig. 2 was a human protein while both PP2C ζ and PP2C η were murine proteins. These observations raised a possibility that either PP2C ζ or PP2C η was the ortholog of human NERPP-2C. However, the data base search indicated that NERPP-2C had a murine ortholog (GenBank™, AK040194), which was different from either PP2C ζ or PP2C η . In addition, both PP2C ζ and PP2C η had human orthologs (GenBank™, human PP2C ζ : BC011803; human PP2C η : AK056894). These results suggest that PP2C η is a novel member of subgroup 2 of the PP2C family.

To determine whether recombinant PP2C η possessed protein phosphatase activity, MBP-PP2C η was expressed in *Escherichia coli* and purified with amylose resin (Fig. 3A). The purified MBP-PP2C η , whose molecular size was 95 kDa on SDS-PAGE, exhibited a Mn²⁺-dependent protein phosphatase activity when phosphorylated α -casein was used as the substrate. Use of 10 mM MgCl₂ in the assay mixture resulted in only a marginal effect on the phosphatase activity (Fig. 3B, left panel). Importantly, the specific activity of MBP-PP2C η was only 4% of that of MBP-PP2C α in the presence of MnCl₂, suggesting that PP2C η and PP2C α act on distinct substrates in vivo (Fig. 3B, right panel). The phosphatase activity was not affected by 1 μ M okadaic acid (OA) (data not shown). Interestingly, PP2C ζ also had a relatively low activity (27% of the activity of PP2C α) against α -casein [10]. These observations may suggest that the sequence difference in motif I between subgroups 1 and 2 contributes to the determination of substrate specificity of PP2C family members.

Northern hybridization was performed on mRNA extracted from mouse tissues to determine the tissue distribution of PP2C η mRNA. A 1.8-kb mRNA was observed in all mouse tissues tested, suggesting that PP2C η is ubiquitously expressed in a variety of tissues (Fig. 4). The signal was the strongest in testis and modest signal was also observed in lung, kidney and brain.

To determine the subcellular localization of PP2C η , we expressed HA-PP2C η in 293IL-1RI cells and immunostained the cells with anti-HA antibody. Confocal microscopic analysis indicated that the exogenous HA-PP2C η was localized mainly to the cell nucleus, although marginal staining was also observed in the cytosol. This result raises the possibility that the putative NLS of PP2C η does in fact play a key role in determining the subcellular localization of PP2C η (Fig. 5). These results, together with the evidence that PP2C η has an extremely low activity against α -casein when compared with PP2C α , may suggest that PP2C η dephosphorylates a unique substrate(s) in

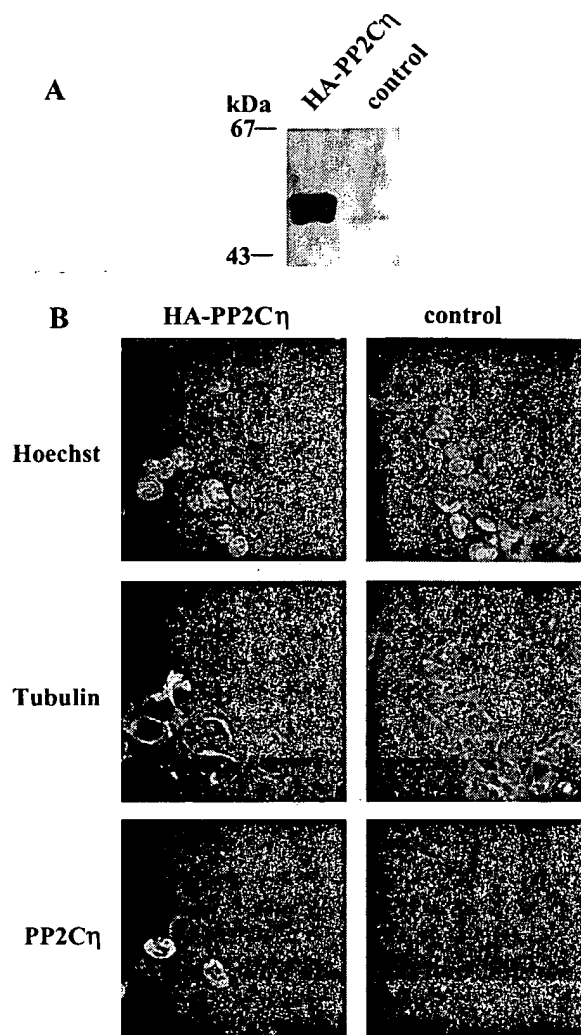


Fig. 5. Subcellular localization of PP2C η expressed in 293IL-1RI cells. (A) 293IL-1RI cells were transfected with the pCX-HA-PP2C η construct (lane 1) or with pCX vector alone (lane 2). Ten micrograms of the cell extract was subjected to 10% SDS-PAGE and immunoblotted with anti-HA antibody. Lane 1, a 55-kDa protein band corresponding to HA-PP2C η was detected. (B) The transfected cells were subjected to indirect immunofluorescence analysis using anti-HA antibody (bottom panels) and anti- α -tubulin antibody (middle panels). The cells were counterstained with Hoechst 33258 to visualize the nuclei (top panels).

the cell nucleus. Further studies are required to determine the physiological functions of this novel PP2C family member.

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